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The ten classes of polymeric phase transitions: their use as models for self-assembly

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Abstract

A brief overview of the ten classes of polymer phase transitions is given. In each case the basic physics underlying the transition is given. Special attention is devoted to the polymer threading a membrane transition (PTM) since it allows us to understand the reason for the occurrence of the five classes of transition unique to the isolated polymer molecule. They are the PTM transition; the helix to random coil transition; adsorption; equilibrium polymerization/one-dimensional crystallization; the collapse transition. The five classes of transitions of interacting polymers are liquid crystals/plastic crystals; glasses; crystals; liquid–liquid polymer transitions; soaps–block copolymers/membranes–micelles–vesicles. A classification is made of the coupling of these transitions to one another in pairs, triplets, etc. and it is observed that the number of kinds of such transitions is in the thousands. Because of the five transitions unique to polymers it is argued that the class of materials richest in the occurrence of phase transitions are polymers. Self-assembly is viewed essentially as materials undergoing phase transitions. It is evident that of all materials, polymers express self-assembly in fullest measure. A classification scheme is given for self-assembled structures both in biology and as a technology opportunity. The paradigm developed in this paper enriches polymer science by revealing the existence of a large number of problems awaiting solution. This paradigm also provides a route towards understanding biological self-assembly. © 1999 Elsevier Science Ltd. All rights reserved.

Keywords: Polymer phase transitions; The ten polymer phase transitions; Biological self-assembly; Biopolymers; Structure inducing phase transitions

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1. Introduction

If one looks about at the various materials that surround us we see that a large number are polymeric. All living things, both plant and animal and their products such as wood, paper and food, the clothing we wear, whether natural or synthetic, plastic containers and vinyl floors, paint, extruded or molded plastic parts, and many others are all polymeric. We would have a real foothold in materials science if we understood why these various polymer structures exist.

It is the contention of this polymer scientist that polymer materials have a richness of structure that is unequaled in any other class of materials and that this structure arises from the many thermodynamic phase transitions that occur in polymer materials. This is shown by listing and describing the ten broad classes of polymer phase transition phenomena in Sections 2.1.2 to 2.2.7, (only five of these transitions have counterparts in non-polymeric materials), by discussing the root cause of this increased complexity in Section 2.1.2, and by discussing how these transitions couple in pairs, triplets, etc. in Section 3. By obtaining a basic understanding of polymer structures as arising from phase transition phenomena we will understand the basic physics of most of the structures with which we have daily contact.

A brief history in chronological order of the initial basic understanding of the ten transitions is appropriate. (1) In the early 1940s, Flory [1,2] and Huggins [3–5] using methods developed by themselves and others (a good history of the development of the theory of polymer solutions is given in Ref. [6]) treated polymer–solvent blends and polymer–polymer blends. The basic understanding behind phase separation in these liquid polymer blends was the same as that for blends of low molecular weight materials. The transitions are basically first-order except near critical and tri-critical points where they can be of higher order. (2) In 1949, Onsager showed [7] that the basic cause of the isotropic to nematic phase transition in lyotropic liquid crystals was the inability of rigid rod molecules to pack at random when their concentration in solution exceeds a certain critical value. The transition is usually weakly first-order. (3) In 1949, Flory showed [8] that the competition between the energy of attraction of monomers wanting to collapse a polymer and the entropically favored expanded state, which occurs because both excluded volume and random placement of monomers favors the expanded state, results in a collapsing of the polymer as the temperature is decreased. The transition is second-order for collapse in a low molecular weight solvent [9] but can be first-order if the collapse occurs in a high molecular weight polymer solvent [10]. (4) In 1956–1958, Gibbs [11] and Di Marzio [12,13] developed an equilibrium theory of glasses by observing that certain molecules do not have a low temperature crystalline phase. For these molecules the low temperature equilibrium phase must be the amorphous phase and by evaluating the statistical mechanics of such systems they discovered that the configurational entropy approached zero at a finite temperature. By identifying this temperature with the glass transition the Kauzmann paradox [14] was resolved. (5) In 1960, Lauritzen and Hoffman [15] and in 1961, Frank and Tosi [16] developed an explanation of chain-folded polymer crystals formed from the melt. Sanchez and Di Marzio extended the treatment to explain molecular weight and concentration dependencies [17,18] as well as fractionation effects [19] when polymers crystallize from dilute solution. (6) In 1959–1961, Tobolski and Eisenberg [20–22] developed a mean-field treatment for living polymers. The non-mean-field work of Wheeler and associates [23,24] should also be mentioned since they were able to show that the transition was second-order. Simple models of polymerization give first-order transitions at the ceiling temperature. See Section 2.1.4. (7) The helix to random coil transition was developed simultaneously by Zimm and Bragg [25] for polypeptides and by Gibbs and Di Marzio [26] for polypeptides and DNA. Zimm [27] in 1961 gave a definitive treatment of the DNA problem which showed it to have a second-order transition, and Applequist [28] treated the 3-stranded collagen molecule which displays a first-order transition. (8) In 1965, Di Marzio and McCrackin [29] showed that an isolated polymer attached to a surface at one end, and whose monomers were attracted to the surface displayed a second-order transition for the case of a body-centered cubic lattice. Rubin [30,31] showed that other lattices also gave second-order transition behavior. (9) In 1997, Di Marzio and Mandell [32] showed that a polymer threading a membrane or partition separating two liquids displays a first-order transition. (10) Finally, there is the very broad class soaps–diblock copolymers/membranes–micelles–vesicles. The basic feature in these systems is the amphophilic character of the molecule. The two discordant parts of the molecule try to phase separate but are prevented from moving too far apart by their covalent connector. Many micro and nonoscale structures result such as the neat, middle and isotropic phases in soaps which correspond directly to the lamellar, cylindrical and spherical phases in block copolymers. There seems to be little to differentiate the soaps from the block copolymers except for molecular weight. The classification of the soaps which dates from the work of Luzzati et al. [33] and Ekwall et al. [34–36] is applicable to block copolymers as well. The recent classifications of Thomas [37] are more comprehensive in that several new phases are discovered.

Books have been written on eight of the ten phase transitions. Books on the collapse transition and the polymer threading a membrane transition have not yet appeared. So, what does this manuscript contribute? We believe that this manuscript contains an overview of the ten polymer transitions and especially of the interrelationships among the transitions that does not exist anywhere else. Sometimes one does not see the forest for the trees. Instead of being like a bird that always lives in one tree, never straying far from it, we seek, in intention at least, to soar above the canopy of the forest. This overview allows us to see the interrelations among the transitions and to understand self-assembly as being basically nothing more than phase transition phenomena. This statement in no way implies that we are anywhere near solving the many problems of self-assembly. Rather our classification schemes show that many thousands of person-years of work remain. The very existence of a classification provides a guide to future work. With this work we now have an overview and paradigm on which to base our future discussions.

The outline of this paper is as follows. In Section 2 we discuss each of the ten classes of phase transitions separately. In each case the basic physics responsible for the transition is discussed, sometimes with a simple mathematical model that captures the essence of the physics. We also show how the transitions relate to each other. Liquid crystals and glasses are shown to be two sides of the same coin; in both cases the transitions occur because of configurational entropy considerations. The five different transitions possible to an isolated polymer have a common cause which is elucidated in Section 2.1.1. Section 3 discusses the coupling of the transitions with one another. The classification will enable us to detail the vast number of unsolved problems requiring future study. Section 4 stresses that the kinetics and pattern formation aspects of the various phase transitions are subjects hardly touched on by the science community. In Section 5 the various ways to control the size and shape of the various phases are listed. Section 6 suggests that since self-assembly is essentially nothing more than phase transition phenomena it should be possible to self-heal by cycling temperature, pressure, chemical potentials and the other intensive variables of thermodynamics such as the electric and magnetic fields and the mechanical stress. Section 7 investigates the important area of biological self-assembly while Section 8 discusses self-assembly as a technology opportunity. In Section 9 we try to circumscribe what we have done by discussing self-assembly as an aspect of complexity physics. Additionally, two speculative comments on life-forms are made. Finally, in Section 10 we end with a discussion.

2. The ten phase transitions

The first transitions are within an isolated macromolecule. Each of these classes of transitions displays a first-order and/or a second-order transition in the Eherenfest sense. If any of the extensive thermodynamic quantities volume, energy, entropy or number of moles shows a discontinuity as a function of the intensive quantities pressure, temperature or chemical potential then we have a first-order transition in the Eherenfest sense. A second-order transition occurs if there is no discontinuity in the extensive quantities but the derivatives of the extensive quantities show discontinuities. As we shall see the

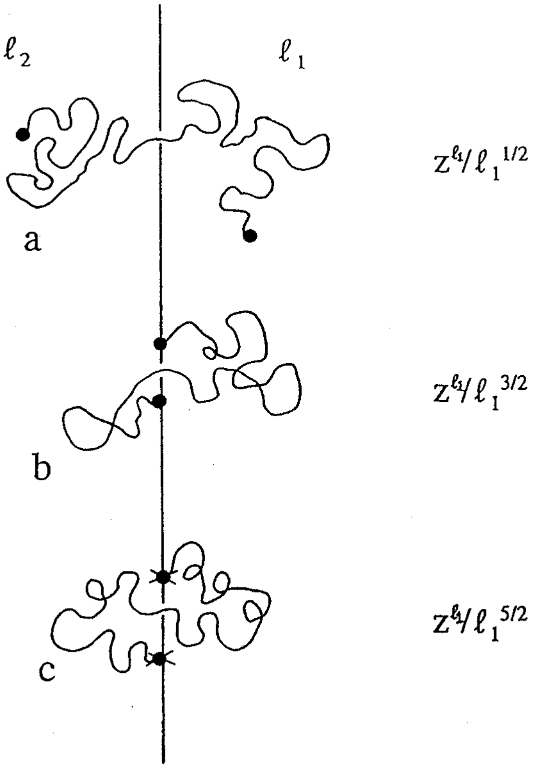
ℓ_2
ℓ_1
$z^{\ell_1}/\ell_1^{1/2}$
a
$z^{\ell_1}/\ell_1^{3/2}$
b
$z^{\ell_1}/\ell_1^{5/2}$
c

Fig. 1. Polymer threading a membrane. A polymer molecule is singly threading, through a small hole, an otherwise impermeable partition separating solutions 1 and 2. In (a) the ends are free, in (b) the ends can roam freely on the surface while in (c) the ends are fixed to the surface. The formulas give the number of configurations of a chain of l_1 monomers attached at one end to the surface and confined in solution 1 as described above. The number of configurations per monomer is z_1 and the attractive energy of the monomer for solution 1 is ε_1. The thermodynamics of this system are easily derived and a first-order transition is obtained.

isolated polymer molecule is a rich source of exactly solvable phase transitions. Additionally, the solutions are easily derived.

2.1. Transitions within one molecule

2.1.1. Polymer threading a membrane [32] (PTM)

Consider a partition or membrane separating two solutions and make one small hole in the partition which is just large enough to allow a polymer molecule to thread through, one segment at a time. Fig. 1 shows three separate possibilities for the ends of the polymer in Fig. 1(a) the ends are free to roam each within their respective solutions. In Fig. 1(b) the ends roam, but only on the surfaces of the membrane while in Fig. 1(c) the ends are fixed on the surface near the hole. The formulas beside each figure give the number of configurations available to a polymer of l_1 bonds tied at one end to a surface with the monomers constrained to lie on the RHS of the partition. These fractional powers of l_1 in the denominators arise because the monomers are constrained to one side of the partition (except by translocating

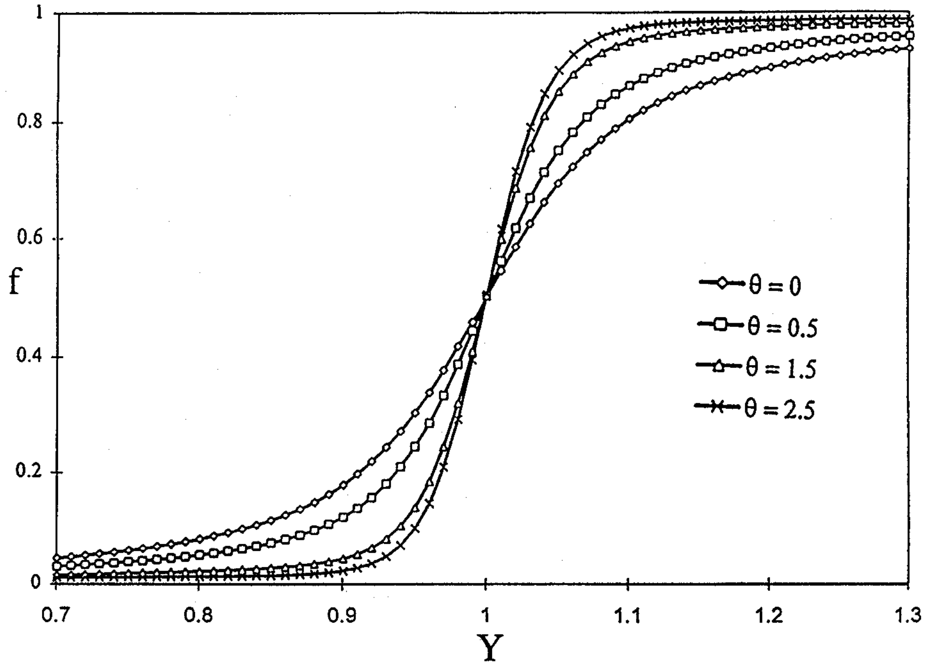

Fig. 2. The fraction of segments residing in Region 1 versus Y, the ratio of partition functions per monomer, for a chain of 50 monomer units suffering various degrees of confinement. The larger the value of $\theta = \theta_1 = \theta_2$ the more the confinement, and the sharper the transition.

through the hole). The canonical ensemble partition function is

$$Q(l,\theta) = \sum_{l_1=0}^{l-1} (x_1)^{l_1}(x_2)^{l_2}/l_2^{\theta_2} l_1^{\theta_1}, \qquad x_1 = z_1\exp(-\beta\varepsilon_1), x_2 = z_2\exp(-\beta\varepsilon_2), l_1 + l_2 = l - 1 \tag{1}$$

where ε_j is the affinity of the monomer segment for solution j, $\beta = 1/kT$, and the θ_j are appropriate to the figure being discussed [38]. The partition is imagined to be infinitesimally thin so that $l = l_1 + l_2$ and the monomer in the hole has zero energy. Finite membrane thicknesses are easily accommodated and result in a constant factor multiplying the RHS of Eq. (1). The thermodynamics of the polymer molecule is obtained by the usual route ($F = -kT\ln Q$, $S = -\partial F/\partial T$, $U = F + TS$). In Fig. 2 we plot the fraction of polymer segments, $\langle l_1\rangle/l$, on one side of the membrane versus $Y = z_1\exp(-\beta\varepsilon_1)/z_2\exp(-\beta\varepsilon_2)$ which is the ratio of monomer partition functions for various values of $\theta = \theta_1 = \theta_2$, and $l = 50$. One sees that the larger the value of θ the sharper the transition. The transition is first-order in the limit of $l = \infty$. To see this consider the $\theta = 0$ case which can be evaluated analytically. We have

$$Q(l) = \sum_{l_1=0}^{l-1} (x_1)^{l_1}(x_2)^{l_2}, \qquad x_1 = z_1\exp(-\beta\varepsilon_1),\ x_2 = z_2\exp(-\beta\varepsilon_2),\ l_1 + l_2 = l - 1 \tag{2}$$

$$Q(l) = [(x_2)^l - (x_1)^l]/[x_2 - x_1] \tag{3}$$

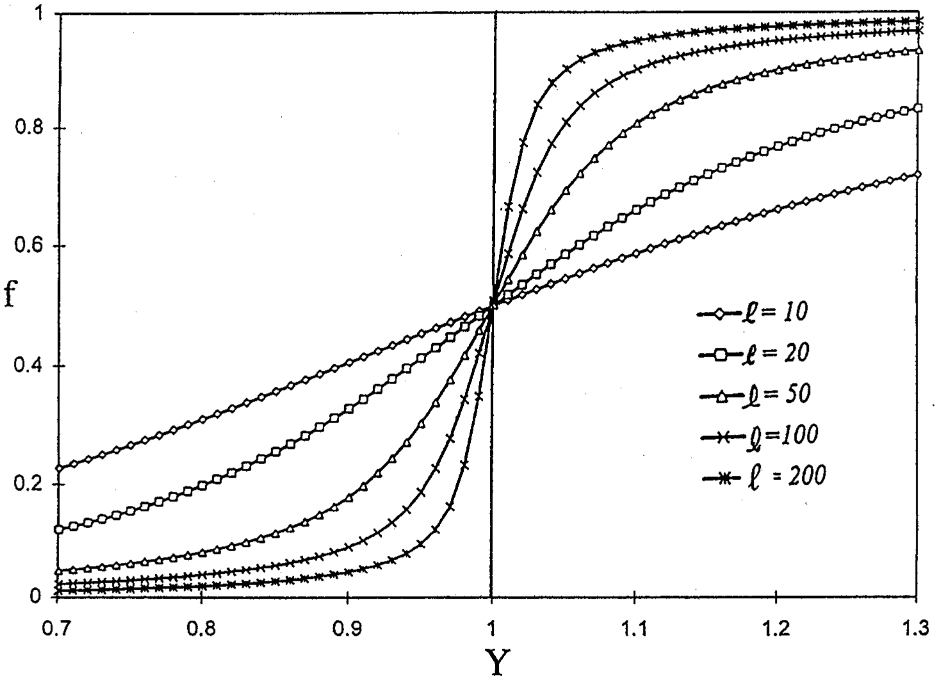

Fig. 3. The fraction of segments residing in Region 1 versus Y, the ratio partition functions per monomer, for polymer chains of different length, l. The value of θ is $\theta = \theta_1 = \theta_2 = 0$. A first-order transition occurs in the limit of infinite molecular weight. From Fig. 2 we conclude that $\theta > 0$ also results in first-order transitions.

which shows a discontinuity at $x_1 = x_2$ when the molecular weight l is infinity. Fig. 3 shows plots of $\langle l_1 \rangle / l$ versus $Y = x_1/x_2$ for various values of chain length l. The transition sharpens with l becoming first-order at infinite molecular weight. Since the $\theta = 0$ case is the least sharp of the transitions as Fig. 2 shows the $\theta > 0$ cases also display first-order transitions. It is a simple matter to show that even when $\theta_1 \neq \theta_2$ the transition is first-order, provided the θs are positive.

Let us now try to understand the reason for the occurrence of the transition. The occurrence of the first-order phase transition is a result of the connectivity of the one-dimensional (1D) polymer chain. We can see this nicely while at the same time gaining an insight into the Gibbs paradox As discussed for example by Tolman [39] or Kubo [40]. Consider a perfect gas of l molecules residing in two volumes of volumes V_1 and V_2. The volumes are separated by a partition with a small channel that allows the gas molecules to translocate. Molecules in region j have an energy ε_j. The partition function for this problem is

$$Q = \sum x_1^{l_1} x_2^{l_2} / l_1! l_2! = (x_1 + x_2)^l / l!, \qquad x_j = V_j \exp(-\beta\varepsilon_j) \tag{4}$$

The fraction of molecules in region 1 is easily calculated as

$$\langle l_1 \rangle / \langle l \rangle = V_1 \exp(-\beta\varepsilon_1) / [V_1 \exp(-\beta\varepsilon_1) + V_2 \exp(-\beta\varepsilon_2)] \tag{5}$$

It is easy to see that this system *does not* have a transition. Indeed when the ε_j are equal to the molecules apportion themselves so that the density is the same in each volume, as expected.

Now consider what our result would be if we did not account for the indistinguishability of the particles and did not divide by the factorial terms. Then we would have Eq. (3) which does show a first-order transition. *Clearly, it is the sequential connectivity along the polymer chain that makes the monomers (molecules) distinguishable from one another and brings on the transition!*

The model presented here suggests that wherever one looks at linear polymers one will see phase transitions in abundance. Indeed this is the case. The transitions that occur in the following four classes of transitions which are discussed in Sections 2.1.2–2.1.5, each occur because the linear connectivity of the monomers makes the monomers distinguishable from each other.

In our analysis we used the canonical ensemble. The grand canonical ensemble is useful when we want to focus on the character of the transition. We have

$$\Xi = \sum Q(l,\theta)\lambda^{l} = \left(\sum (x_1\lambda)^{l_1}/l_1^{\theta_1}\right)\left(\sum (x_2\lambda)^{l_2}/l_2^{\theta_2}\right), \qquad \lambda = \exp(\beta\mu) \tag{6}$$

from which the thermodynamics can be derived [41] for a molecule. Ξ is seen to be a product of Truesdel functions [42]. This form can be used directly to obtain $\langle l_1\rangle$ and $\langle l_2\rangle$.

$$\langle l_1\rangle = \left(\sum j(x_1\lambda)^{j}/j^{\theta_1}\right)/\left(\sum (x_1\lambda)^{j}/j^{\theta_1}\right) \tag{7}$$

$$\langle l_2\rangle = \left(\sum j(x_2\lambda)^{j}/j^{\theta_2}\right)/\left(\sum (x_2\lambda)^{j}/j^{\theta_2}\right) \tag{8}$$

In these formulas μ is not the chemical potential of the solution(s); it is the chemical potential for polymerization. Statistical mechanics tells us that in the limit of infinite molecular weight the grand canonical ensemble gives the same result as the canonical ensemble. From this we see that for infinite $l = \langle l_1\rangle + \langle l_2\rangle$ the ratio $\langle l_1\rangle/\langle l_2\rangle$ passes discontinuously from zero to infinity as $Y = x_1/x_2$ passes from 1^- to 1^+.

2.1.2. The helix to random coil transition in biological macromolecules

The book by Poland and Scheraga [43] has a rather complete treatment of this problem and is also a collection of reprints of pivotal papers. Of the two simultaneously published equivalent treatments that first offered exact solutions of the problem, the matrix method of Zimm and Brag [25] is more difficult to understand but easier to use, while the maximum term method of Gibbs and Di Marzio [26] is easier to understand but more difficult to use. Details can be obtained from the original papers or the book. In this section we shall not give a complete treatment but rather only emphasize those aspects of the problem that determine the order of the transition.

The helix to random coil transition can occur in single-stranded polypeptides [25,26], double-stranded DNA [27] and triple-stranded-collagen [28], and as we shall see the transition goes from being diffuse, to second-order, to first-order as we increase the number of strands from 1 to 3 (see Fig. 4). In each case we model the system as an alternation of helical portions and random coil portions. The helical portions have energy stabilizing the helical structure(s) while the random portion(s) have configurational entropy stabilizing the random coil. The energy of the helical portion is proportional to the helical length. This energy is the energy difference between the helix–solution complex and the random coil–solution complex, only part of which can be ascribed to hydrogen bonds. If the number of configurations of a random coil of n monomers is z^n then the number of configurations of a double-strand of n monomers is $z^n/n^{3/2}$. This expression is obtained from a Gaussian representation of the molecule with the two ends tied

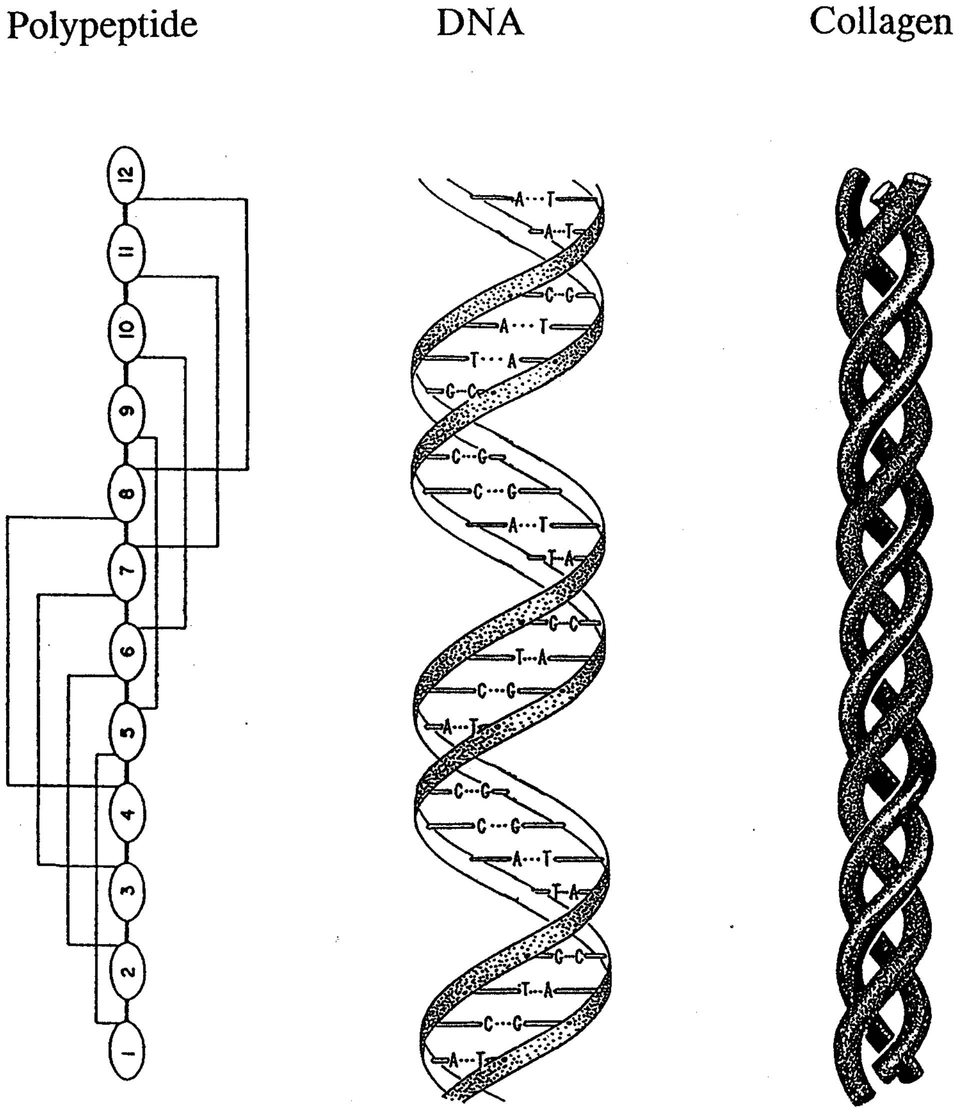
Polypeptide
DNA
Collagen
12
11
10
9
8
7
6
5
4
3
2
1
A···T
A–T
C–G
A···T
T···A
G–C
C···G
C···G
A···T
T–A
G–C
T···A
C···G
A···T
C···G
C···G
A···T
T–A
G–C
T···A
C···G
A···T

Fig. 4. Schematics of the helical portions of a single-stranded polypeptide, double-stranded DNA, and triple-stranded collagen. By breaking three consecutive hydrogen bonds rotation is allowed about the covalent peptide bonds; by breaking the hydrogen bonds between adenine and thymine and/or guanine and cytosine side groups a random coil portion is introduced in DNA; by breaking the hydrogen bonds (not shown) between strands of collagen we also induce an alternation of helical and random coil portions. For the perfect matching model the transition obtained by changing temperature or chemical potential is first-order in collagen, second-order in DNA and diffuse in polypeptides.

together (end-to-end length equals zero). For a k-stranded loop with each strand having length n the number of configurations is proportional to $z^{kn}/n^{3(k-1)/2}$. To obtain this result write the number of configurations W_3 of a denaturated k-stranded loop as

$$W_3 = \int \left[z^n (2\pi n l^2/3)^{-3/2} \exp(-3r^2/2nl^2) \right]^k \mathrm{d}\mathbf{r}. \tag{9}$$

Each strand of n monomers has $z^n(2\pi nl^2/3)^{-3/2}\exp(-3\mathrm{r}^2/2nl^2)$ configurations consistent with the end-to-end length being r. This expression is normalized so that integration over r results in z^n configurations. Integration of Eq. (9) results in

$$W_3 \propto z^{kn}/n^{3(k-1)/2}. \tag{10}$$

Thus the power of n in the denominator is 0, 3/2, or 3 depending on whether we have polypeptide, DNA or collagen molecules. We are now equipped to discuss our model of biological macromolecules as an alternation of loops and helical portions but first we will discuss the simpler zippering–unzippering (ZUZ) model.

The simplest treatment of the helix–random coil transition is the ZUZ model [26,44]. In the ZUZ, model unzippering is not allowed in middle portions of the helix, nor is helix formation allowed in middle portions of the random coil. ZUZ is allowed to occur only at the one interface dividing the helical and random coil portions of the chain. In general this is not realistic although the helical nature of the polypeptide, DNA or collagen chains can shield the internal hydrogen bonds from interchanging with solvent hydrogen bonds. If the solvent molecules are so large that they cannot penetrate the helix then the unzippering of these chains occurs only at the ends and may be treated by the ZUZ model. However, even in this case there is nothing to prevent helix formation within the random coil part of the chain. This model is expected to be realistic only if the unzippering of the helix is fast compared to the nucleation and growth of a helical portion within the random coil portion of the chain. The equations are identical to Eq. (1) with $\theta_2 = 0, z_2 = 1$; and $\theta_1 = 0, z_1 = z$ for single-stranded polypeptides, $\theta_1 = 3/2$, $z_1 = z^2$ for double-stranded DNA (perfect matching model), and $\theta_1 = 3$, $z_1 = z^3$ for triple-stranded collagen (perfect matching model). If one imagines that the unzippering process separates the ends of the random coil strands then $\theta_1 = 0$ for all three cases. In any event the ZUZ model gives first-order transition behavior in all cases.

The ZUZ and the PTM transitions have identical mathematics, but the physical interpretation is very different. In the ZUZ transition one always has the possibility of forming a helical region within the random coil region or a random coil region within the helical region, but the possibility is ignored. With the PTM it is meaningless to talk of region 1 within region 2 or region 2 within region 1.

The more realistic treatment is one in which we model our biological macromolecules as an alternation of loops and helical regions. If our main interest is to determine the order of the transition we can work with the grand canonical ensemble. In this case we have

$$\Xi = \sum (X_1(x_1\lambda) X_2(x_2\lambda))^k, \qquad X_1(x_1\lambda) = \sum (x_1\lambda)^{l_1}/l_1^{\theta_2}, \;\; X_2(x_2\lambda) = \sum (x_2\lambda)^{l_2} \tag{11}$$

$$\Xi = X_1(x_1\lambda)X_2(x_2\lambda)/(1 - X_1(x_1\lambda)X_2(x_2\lambda)) \tag{12}$$

where $X_1(X_2)$ is the partition function of the random coil loop (helical portion). By the use of tags to keep track of monomers in the helical or random coil region we obtain

$$\langle l_1\rangle = \lambda\partial X_1/\partial\lambda(X_1(1 - X_1X_2))^{-1} \tag{13}$$

$$\langle l_2\rangle = \lambda\partial X_2/\partial\lambda(X_2(1 - X_1X_2))^{-1} \tag{14}$$

The new feature in these equations, compared to Eqs. (7) and (8) is that infinite $l = \langle l_1\rangle + \langle l_2\rangle$ occurs when

$$X_1X_2 = 1. \tag{15}$$

This equation determines λ as a function of x_1, x_2, and the ratio

$$\langle l_1\rangle/\langle l_2\rangle = (\partial X_1/\partial\lambda)X_2/(\partial X_2/\partial\lambda)X_1 \tag{16}$$

which can vary continuously as a function of $Y = x_1/x_2$. One should also note the easily proved result that in the limit of large l the canonical partition function Q equals λ^{-l}. The character of the transition now depends on the functional forms of X_1 and X_2. Poland and Scheraga [41] have examined the phase transition characteristics of the transition as a function of θ_1. As they show the transition can be of any order. For double-stranded DNA $\theta_1 = 3/2$ and the transition is second-order while for collagen $\theta_1 = 3$ and the transition is first-order.

It is surely no accident that collagen, the main structural protein of animals, is triple-stranded since three strands are needed to obtain an underlying first-order transition which then serves to stabilize the structure. It is also surely no accident that the packaging of DNA involves molecules other than DNA since naked DNA when undergoing its second-order transition has random coil dimensions that are larger than the cell itself into which the DNA is packaged. These other molecules can act as a third strand which then lowers the character of the transition to first-order thereby allowing packaging.

2.1.3. Adsorption of an isolated polymer

The isolated polymer on a surface problem is interesting in its own right and as a foundation onto which a treatment of interacting polymers near surfaces can be built. In its own right: a recent book [45] devoted to the problem of polymer interfaces has a chapter [46] in which the isolated polymer at a surface problem is solved by five separate methods. As a foundation for interacting polymers: Scheutjens and Fleer [47,48] and Fleer and coworkers [49] have succeeded in solving the many polymers at an interface problem and have successfully applied their methods to many polymer and biopolymer problems. The importance and wide applicability of the general problem of polymers at a surface can be judged by examining a list of 52 applications in Ref. [46]. An additional, more recent, and important application of the isolated polymer problem is to critical chromatography [50,51]. In this subsection we will first give a proof that the isolated polymer at an interface problem is isomorphic to the DNA problem and therefore displays a second-order transition in the Ehrenfest sense. Then we will outline the original [29] and simplest method that gives complete information and describe some of the quite surprising results.

The middle portion of a polymer adsorbed onto a plane surface is an alternation of trains and loops, while at the ends we have two tails extending from the surface, or one tail if have tied down one end as in a brush. By definition, each segment of the train contacts the surface and if we image a cubic lattice model of coordination number z then the weight of a train is $((z - 1)\exp(-\beta\varepsilon_h))^n$ where n is the number of monomers forming the train, or if we imagine the train to be stiff and straight the factor $(z - 1)$ is absent. Thus the train portions of an adsorbed polymer have the same mathematical form as the helical portions of DNA. We will now show that the loops have the same dependence on monomer number as the loops (denatured portions) of DNA. We begin with the expression for the number of configurations of a random walk polymer attached to a plane surface and confined to one side of it. It is [46]

$$W(\mathbf{r},n) = (3hz^n/nl)(2\pi nl^2/3)^{-3/2}\exp(-3\mathbf{r}^2/2nl^2) \tag{17}$$

where $\mathbf{r}^2 = x^2 + y^2 + h^2$, and h is the height above the plane surface. By integrating over x and y and remembering that we can locate the end only to within a volume of l^3 we obtain for a loop whose one end is fixed at the origin and whose other end is free to roam on the surface

$$W_{\text{loop}} = 2z^n/n^{3/2} \tag{18}$$

which has the same n dependence as DNA loops. Eq. (17) can also be used to derive the two other equations displayed in Fig. 1. For a tail we have from Eq. (17)

$$W_{\text{tail}} = 0.7z^n/n^{1/2} \tag{19}$$

Thus for polymers, for large molecular weight when we can neglect end effects, the polymer adsorption problem is isomorphic to the DNA problem. It therefore displays a second-order transition in the Ehrenfest sense just like DNA.

Perhaps the simplest exact treatment of an adsorbed polymer molecule is the original treatment [29]. One imagines a 1D random walk to begin at the origin and to be confined to the positive x axis by a barrier. This problem is simply solved. The relevant mathematics are contained completely in Feller's book [52] on probability theory. The crucial step [53] is the use of the reflection principle which allows us to express the number of configurations in the presence of a barrier in terms of the numbers in the absence of a barrier. Suppose the two ends of a random walk are located at points A and B on the same side of the barrier which is located at the origin. The number of walks from A to B that do not touch or cross the origin is equal to the total number of walks from A to B in the absence of the barrier minus the total number of walks that touch or cross the origin. This latter number is by the reflection principle equal to the number of walks from A′ (the reflection of point A through the origin) in the absence of a barrier. Thus the problem of a walk in the presence of a barrier is related to the number of walks in the absence of a barrier. By weighting each time the walk touched the surface with an energy ϵ the partition function for this one dimensional problem is easily obtained and the thermodynamics evaluated [29]. But it is clear that we have also solved the adsorption problem for the body centered cubic lattice as well. The only difference is that in the 1D problem there is one way to step away or to step towards the origin while in the d-dimensional bcc lattice there are 2^{d-1} ways to step away or to step towards the surface. Rubin [30,31], using recurrence relation techniques has solved the problem of a polymer molecule near a surface for a variety of lattices. In all cases there is a second-order transition. Fig. 5 shows the adsorption curves for various lattices. The transition point is given by $\varepsilon/kT = \ln(2/(2-a))$ where ε is the contact energy of a monomer for the surface and $1 - a$ is the fraction of steps running parallel to the surface.

Some of the results are not intuitive and quite surprising. This lack of intuition derives from the lack of intuition that most people have for the conclusions of probability theory itself, as Feller nicely explains in his book [52]. This being the case we can expect to be surprised!

If one end is tied to the surface, the other end free, then when there is no monomer surface attraction the normal polymer scientist would expect the number of contacts with the surface to be proportional to

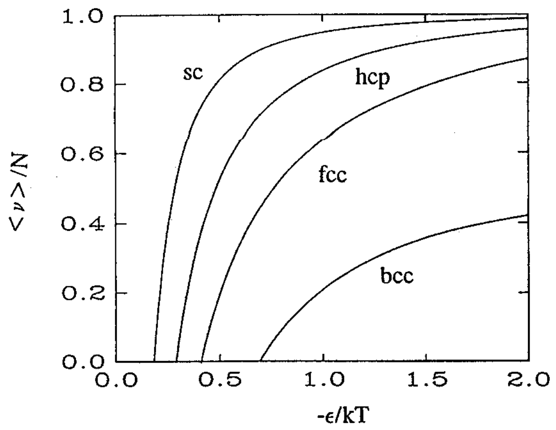

Fig. 5. Polymers confined to a lattice and lying on one side of a surface, with one end fixed to the surface, undergo a second-order transition as the strength of the attraction of the monomers for the surface is increased. A monomer has an energy zero unless it is on the surface in which case the energy is ε. The lattice types label the curves. sc = simple cubic; hcp = hexagonal close-packed; fcc = face-centered cubic; bcc = body-centered cubic.

the square root of molecular weight. In reality for an infinite chain the expected number of monomer contacts with the surface is only 1! At the transition temperature the expected number of contacts is indeed proportional to the square root of molecular weight but the fraction of contacts is zero as Fig. 6 clearly shows; in the adsorption region the expected number of contacts is proportional to molecular weight. In the adsorption region the monomer density decreases exponentially as we go from the surface and the adsorption profile is independent of molecular weight for modestly large molecular weight, while in the desorption region the monomer density increases as we go out from the surface, reaching a maximum at a distance which is proportional to the square root of molecular weight (see Fig. 7). The transition point occurs when the density gradient is zero and is therefore given by the reflecting boundary condition.

Klushin et al. have treated the adsorbed polymer exactly in the Gaussian limit including a consideration of the behavior of the polymer under a force applied to one end [54,55]. Significantly, they have shown that Landau theory fails [55]. This is an example of an exact treatment showing that seemingly reasonable assumptions about complex systems are often wrong.

An already dated review of an isolated polymer near a surface gives 52 applications [46]. There are more. Because of the large number of applications it is important to solve the problem of an isolated polymer at a surface in all its variations. Some of them are: different shaped surfaces [56], chemically inhomogeneous surfaces [57–59], fractal [60] and rough [61] surfaces, long-range interaction energies [62], accounting for the energetics of monomer–monomer, monomer–solvent, monomer–surface, solvent–surface interactions [49], the effects of excluded volume [63,64], polymers of various architecture [65], vis. rings, combs, stars, polymers of different composition, such as block and random copolymers, kinetics of adsorption and desorption, kinetics of adsorption into pores [66], stagnant or flowing solutions, liquid surfaces [67], and two-phase solvents. Each one of these variations has application to important problems.

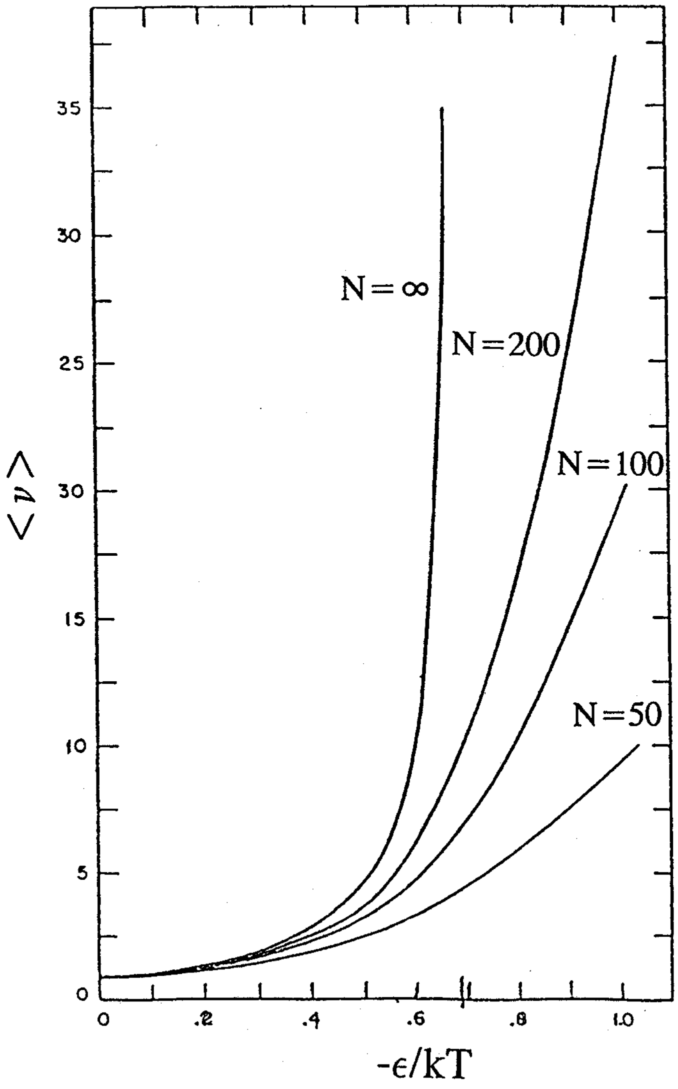

Fig. 6. Number of contacts with the surface versus monomer energy of contact with the surface for various molecular weights. Although the fraction of contacts in the desorbed region is zero (for infinite molecular weight) the actual number of contacts is finite as this figure shows. For 1d the number of contacts varies from 1 when the adsorption energy is zero to $(\mathrm{MW})^{1/2}$ when the adsorption energy has the value appropriate to the transition point ($-\varepsilon/kT = \ln 2$, which is the reflection boundary condition).

2.1.4. Equilibrium polymerization/1D crystallization

A unique feature of this problem is that a suitably restricted model can be solved exactly in both its equilibrium and kinetic aspects [68,69]. The model consists of an ensemble of polymer chains immersed in a bath of monomers. These chains which are sufficiently far apart to avoid mutual interference grow or ungrow by addition (deletion) at one end with rate constants α_j (β_j), with j being the length of the chain in monomers. One does not allow the chains to break in middle positions or to come together to form

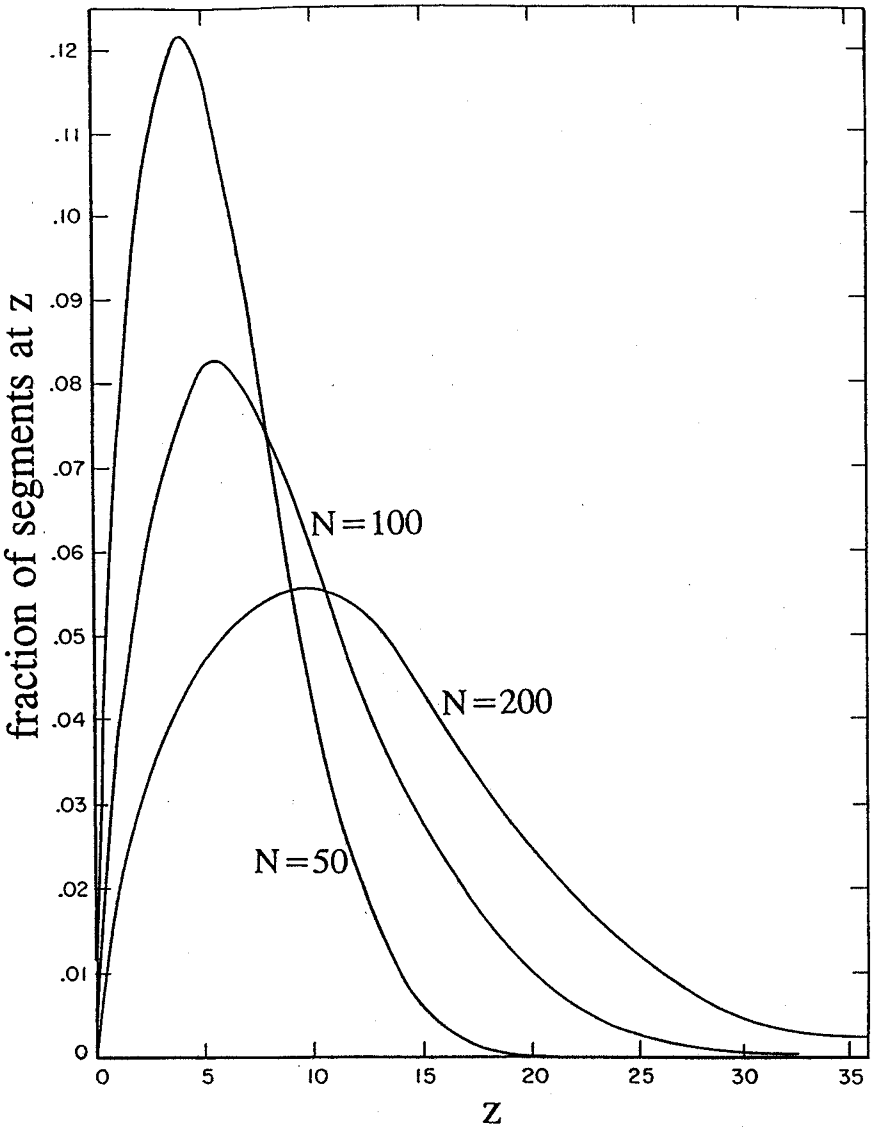

Fig. 7. Polymer density versus distance from the surface for the case when the adsorption energy is zero (desorption region) for various molecular weights. The location of the maximum density varies $(MW)^{1/2}$. In the adsorption region (not shown) the polymer density is maximum at the surface and decays exponentially from the surface.

larger chains; only addition (deletion) of monomers at the one growing end is allowed. The chains started growing initially at N_0 locations on a substrate labeled $j = 0$.

This model forms the basis on which virtually all of polymer crystallization theory rests. The kinetic part of the problem is discussed in Section 4.1, and in Section 2.2.3 application is made to polymer crystallization. Here we discuss equilibrium. If adding the jth monomer changes the energy by ε_j then the grand canonical potential is

$$\Xi = \sum \exp\left(-\beta\left(\Sigma\varepsilon_j - n\mu\right)\right). \tag{20}$$

When the ε_j are equal the summation is easily performed

$$\Xi = X(1 - X^{\infty})/(1 - X), \qquad X = \exp(-\beta(\varepsilon_j - \mu)) \tag{21}$$

which again shows that the chain becomes infinitely long when μ exceeds a critical value, $\mu > \mu_c$, and the chain is finite if $\mu < \mu_c$. Thus, the transition is first-order. The connection between the critical temperature and the rate constants is given by the principle of detailed balance. At equilibrium

$$N_j\alpha_j = N_{j+1}\beta_{j+1} \tag{22}$$

where α_j is the rate of adding and β_j is the rate of taking off a monomer at the jth site. Since the N_j are known from Boltzmann's law we have

$$N_{j+1}/N_j = \exp(\beta(\mu - \varepsilon_{j+1})) \tag{23}$$

$$\alpha_j/\beta_{j+1} = N_{j+1}/N_j = \exp(-\beta(\mu - \varepsilon_{j+1})) \tag{24}$$

which relates the rate constants to the thermodynamics. This formula is useful when determining the rate constants.

The above treatment is valid when the N_0 initiating sites are in fixed positions and the chains created are straight, fixed in orientation and sufficiently dilute that they do not interact. When the initiating sites are not as described (they may be rings for example) and the chains interact then the problem is more complicated. In this case the mean field methods of Tobolski and Eisenberg [20–22] and the more exact methods of Wheeler and associates [23,24] must be used. The transition becomes second-order. A recent review is given by Greer [70].

2.1.5. Collapse transition

Flory [8] was the first to quantify the competition between the attractive interaction among monomers wanting to collapse the polymer onto itself and the entropy of the polymer chain wanting to expand the polymer. His treatment gave the proper (accurate but not exact) 6/5ths law regarding the end-to-end dimension, $\langle R^2\rangle = An^{1.2}$, in the expanded region but his method did not establish the character or existence of the transition. Perhaps the simplest approach that both displays the transition and retains the flavor of the original Flory ideas is to deal directly with the more fundamental probabilities [9] rather than the thermodynamic properties derived from them as Flory did. We now give an abbreviated version of this approach.

The probability of a polymer chain having an end-to-end length R is given by the product of three factors

$$W = [R^2\exp(-b^2R^2)]\left[\prod_{j=0}^{n-1}(1 - jl^3/R^3)\right][\exp(-n\chi(1 - nl^3/R^3))] \tag{25}$$

where the first factor is the Gaussian distribution function for the end-to-end length, the second factor corrects for excluded volume and the third factor gives the energy. The notation is standard: $b^2 = 3/2nl^2$,

l^3 is the volume of a bead monomer, n the number of monomer units and χ is the χ-parameter. The first and third terms are clearly correct and do not need discussion although they are approximations that can be improved. To understand the second term imagine that the polymer is being built up one monomer at a time. The kth monomer can be placed if there is no interference from monomers placed previously on the chain. To evaluate the probability of successful placement of the jth monomer imagine that the previous $(j-1)$ segments are distributed at random in the volume of the sphere. This gives the factor $(1 - jl^3/R^3)$ and the product of these factors constitutes the second factor of Eq. (25).

From Eq. (25) we can find the expectation value of R through the relation $\langle R^2\rangle = \int R^2 W \mathrm{d}R / \int W \mathrm{d}R$, but this cannot be done analytically. Instead we find the value of R which maximizes W (actually [9] RW) by differentiating Eq. (25) to obtain

$$\alpha^5 - \alpha^3 = -n^{1/2}[n\alpha^6(\ln(1 - n^{-1/2}\alpha^{-3}) + n^{-1/2}\alpha^{-3}) + \chi], \qquad \alpha = R/(nl^2)^{1/2} \tag{26}$$

which reduces to the Flory result for large R.

$$\alpha^5 - \alpha^3 = n^{1/2}[1/2 - \chi] \tag{27}$$

Thus, the $R^2 = An^{1.2}$ law is obtained. Additionally, Eq. (26) can be solved through the transition to obtain the law $R^2 = Bn^{2/3}$ in the collapsed region. This does not mean however that the collapsed phase has unit monomer density; it is in fact less than unity. Fig. 8 gives R^2 for various values of n while the plot of the energy in Fig. 9 shows that the transition is second-order.

An interesting result occurs when the solvent is polymeric. Then, depending on the relative molecular weights and energetics, the transition can be first-order as well as second-order [10].

Because of its simplicity the method is adaptable to other situations in which excluded volume plays a significant role. For example a polymer between two plates can be solved by the same procedure; one needs the results of a random walk for the particular geometry in which characteristic dimensions appear (corresponding to the first factor in Eq. (25)), one needs a term analogous to the second factor which expresses the excluded volume contribution in terms of the characteristic polymer dimensions, and one needs an energy term expressed in terms of the same dimensions. We expect the goodness of the approximation to carry over to this case as well. A recent review of collapse in polymers in given by Grosberg and Kuznetsov [71].

Discussion of the five isolated molecule transitions: Four of the above treatments are exact solutions to realistic models. Only the collapse transition is approximate, because excluded volume is treated. If excluded volume were treated in the other four cases they would be also be approximate treatments. The author is aware of no other material for which there are as many exactly solvable models. Certainly there are no materials for which their phase transitions can be treated exactly in such a simple fashion.

The above five treatments have the common feature that they each display phase transitions of first- or/and second-order. As shown in Section 2.1.1 these transitions are directly attributable to the connectedness of the monomer units into a flexible infinitely long chain. Thus, small changes in the intensive thermodynamic variables, T, P, μ_j can result in drastic changes in the polymer molecule. This is exactly what is needed in biological cell division. The cell needs to make many different kinds of structures repeatedly. The five transitions plus their coupling (see Section 3) to

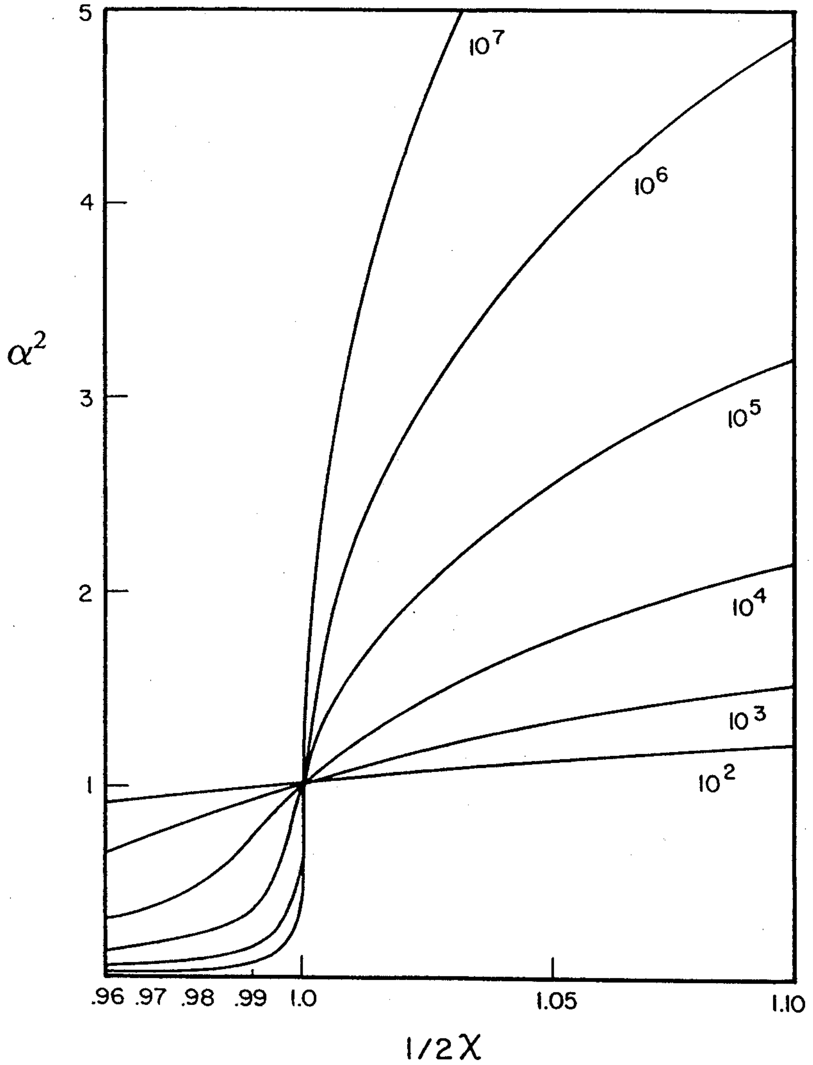

Fig. 8. The normalized size of a collapsing polymer ($\alpha = R/R_0$) versus normalized temperature for various molecular weights. In the expanded region R^2 varies as $(\mathrm{MW})^{6/5}$ while in the collapsed region R^2 varies as $(\mathrm{MW})^{2/3}$.

themselves and to the other five transitions discussed in Sections 2.2.1–2.2.5 allow this. To this author the molecules of life must necessarily be polymeric; it is no accident that DNA, RNA, proteins—the molecules of life—are each polymeric. Polymers are the only class of materials that have a sufficient number of phase transitions to accommodate the required structures of life-forms.

In the above treatments we did not discuss the effect of placing a force on and end of the polymer. For the adsorption problem it is quite plain as Di Marzio and Guttman show [72] using a lattice model, that for each temperature there is a critical value of force perpendicular to the surface which will completely

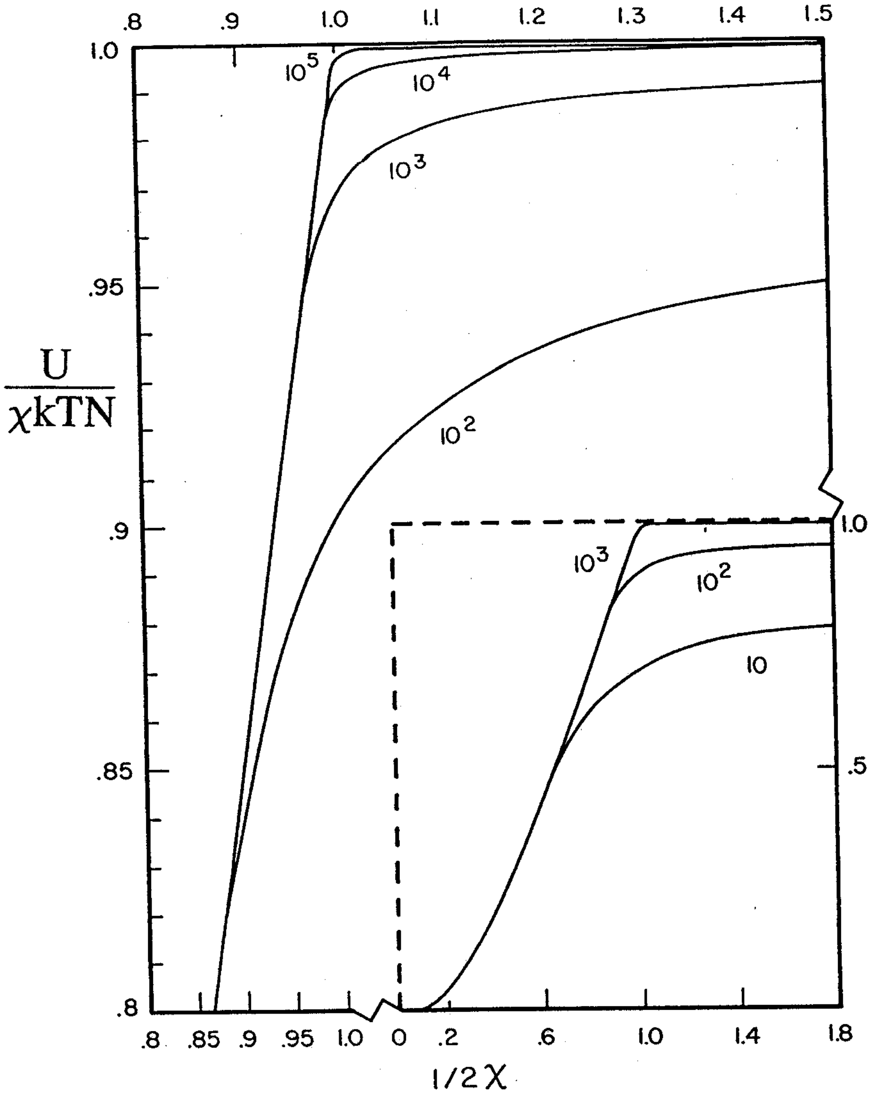

Fig. 9. The normalized energy per monomer unit of a collapsing polymer versus normalized temperature for various molecular weights. The transition displayed here is second-order but if the polymer were collapsing in a field of other polymers, rather than in low molecular weight solvent as displayed here, the transition could be first-order.

remove the chain from the surface. The transition is first-order. Klushin et al. [54,55] have an interesting continuum treatment of the polymer on a surface which includes a force on one end. By treating this problem exactly (the polymer is represented as a Gaussian coil) they show that Landau theory fails, for this problem at least. One of the virtues of doing the simple polymer problems exactly is that they often provide a benchmark against which more difficult problems that cannot be solved exactly can be compared. In this case the venerable Landau theory (a clear discussion of Landau theory is given by Domb [73]) is shown to have limitations that are not often realized nor appreciated by the larger science community.

2.2. Transitions within collections of molecules

2.2.1. Liquid crystals/plastic crystals

Onsager was the first to assert that hard core rigid rods formed nematic phase liquid crystals even when there is no energy favoring parallel alignment [7]. He proved by use of a virial expansion that as the concentration of rigid rods increased beyond a critical value the rod-solvent system would convert from the isotropic to nematic phase. In dilute solution rigid rods are unaffected by neighbors and can orient in any direction. However as the rigid rod concentration is increased, the neighbors to a rigid rod prevent it from achieving all of its orientations. The rod is frustrated. Flory, using lattice model methods, calculated that this frustration becomes important at $rV_r = 8$ where r is the ratio of length to width of the rod and V_r is the volume fraction of rods [74]. Later estimates [75,76] give a value closer to 4 rather than 8. This inability of rigid rods to pack at random occurs at all levels of size, from molecules to logs. Consider the following examples: (1) A log jam on a river is alleviated by making the logs parallel. (2) No maker of dry spaghetti would ever sell boxes of randomly oriented strands. The volume of the box would be too large and expensive relative to the price of the spaghetti, to say nothing of transportation costs. Rather, the parallel strands occupy close to unit density and are cheaply packaged and transported. (3) One can get a good feeling for the packing problem in two dimensions by placing pencils on a desktop first in parallel and then in random order. (4) Imagine the difficulty a school of gar fish would have if the individual fish were oriented at random. At high densities they would get stuck. (5) The volume of a disheveled head of hair is larger than a combed head because combing places the hair in more parallel alignment allowing it to occupy less volume. There are many more examples at all levels of size scale.

These ideas were made quantitative by use of orientation-dependent Flory–Huggins (FH) like lattice statistics [77–79]. Recent computer modeling shows that the assumption of a lattice does not affect results adversely[1]; provided we count configurations on the lattice correctly. When lattice model calculations err it is because the calculations of the number of configurations on the lattice is done incorrectly; not because we used a lattice. We shall now give a detailed derivation of the number of ways to pack rigid rods on a 2D square lattice. The generalization to arbitrary dimension is trivial.

The calculation proceeds by placing the rods one at a time onto the lattice while keeping a running count of the number of configurations. In order for the calculation to be self-consistent, as it is, the result will not depend on the order of placement. We have N_x (N_y) rods of length r lying in the x (y) orientation. We shall place the N_x rods and then the remaining N_y rods on a lattice of $N_x + N_y + N_0 = N$ sites, N_0 being the number of unfilled sites remaining after all the rigid rods are placed. After j rods have been placed in the x orientation the first segment of the $(j+1)$th rod can be placed in any of $N - jr$ locations. To lay down the remaining $(r-1)$ segments of this rod we need the $r-1$ adjacent contiguous sites lying in the x orientation to be empty. In the Flory version of FH lattice statistics one would spread the previously placed jr segments randomly. The probability of a successful step would be equal to the probability that a site is empty which is $p_s = [N - jr]/N$. The probability that $(r-1)$ contiguous sites are simultaneously empty is $p_s^{(r-1)}$. However a more accurate counting is needed for the orientation dependent statistics. The place from which we step is a neighbor to the place into which we step. So the number of neighbors to holes (empty sites) compared to the number of neighbors to occupied sites is relevant. The number of neighbors to holes in direction x is $(N - jr)$, while the number of neighbors to rods in the x direction is j since each rod has only one neighbor in the x direction. The probability of a successful step p_s plus the probability of an unsuccessful step is 1. We then have two equations

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[1] The author believes this is a consensus opinion.

$$p_s + p_u = 1, \tag{28a}$$

$$p_s/p_u = [N - jr]/j \tag{28b}$$

from which we obtain

$$p_s = [N - jr]/[N - j(r-1)] \tag{29}$$

and the probability that (r-1) contiguous sites lying in orientation x are empty is $p_s^{(r-1)}$. The number of configurations (number of ways to place the $(j+1)$th molecule on the lattice is then given by

$$[N - rj]p_s^{(r-1)} \tag{30}$$

After the N_x rods are placed and k of the N_y rods are laid down in the y orientation we have for the probabilities of successful and unsuccessful placings of the $(k+1)$th rod in the yth direction

$$p_s + p_u = 1, \tag{31}$$

$$p_s/p_u = [N - rN_x - kr]/[rN_x + k] \tag{32}$$

$$p_s = [N - rN_x - kr]/[N - k(r-1)] \tag{33}$$

and the number of ways to place the $(k+1)$th rod in the y orientation is

$$[N - rN_x - rk]p_s^{(r-1)} \tag{34}$$

Notice that the number of neighbors to rods is orientation dependent. If the rods which are already placed on the lattice lie parallel to the direction of step they contribute as mole fractions while if the rods lie perpendicular to the direction of step they contribute as volume fractions. This insight is due to Flory [77].

By multiplying the j-dependent product of terms given by Eq. (30) and the k-dependent product of terms given by Eq. (34) together and taking proper account of indistinguishability of rods in the same orientation we obtain for $W(N_x, N_y, N_0)$ the number of ways to place N_x rods in orientation x, N_y rods in orientation y, an N_0 solvent molecules (or holes) on a square lattice of $N_x + N_y + N_0 = N$ sites.

$$\ln(W(N_x, N_y, N_0)) = -\sum_{k=1}^{2} [N_k \ln(N_k/N) - (N - (r-1)N_k)\ln(1 - (r-1)N_k/N)] - N_0 \ln(N_0/N) \tag{35}$$

It is a simple matter to show that if we replace the upper limit by d then Eq. (35) is valid for all dimensions.

This equation is a useful generalization of the FH results which are valid for isotropic solutions. For an isotropic solution ($N_k = N/d$) we obtain the Huggins result (see Ref. [6; Eq. (3.48)]) for rigid rods while for one dimension Eq. (35) gives the exact result. Also, it can be shown that for d dimensions and the rods all lying in one orientation the result is exact in the thermodynamic limit. This means that the leading term of an expansion of ln W in powers of $N_r = N_x + N_y$ is the exact result and that all subsequent terms are of lower order. Finally, as an aside, we should mention that if flexible molecules are stretched so that the fraction of bonds lying in orientation k is α_k, then Eq. (35) (with a small correction to the indistinguishability factor) accounts for the interferences among chains with the substitution $\alpha_k = N_k/(N_1 + N_2)$. This allows us to improve the classical theory of rubber elasticity which is a gas-like theory by accounting for the mutual interferences that stretched molecules suffer in their liquid-like state. See Di Marzio [80,81] and Tanaka and Allen [82] for details.

Armed with our reasonably accurate expression for the entropy one can add energies to obtain predictive theories of liquid crystals [83–96]. A nice feature of Eq. (35) is that it is easily adapted to molecules that have both rigid and flexible portions. Although the qualitative features of liquid crystals are well represented by lattice theories with energetics continuous angle models based on generalizations [97] of Maier–Saupe [98–100] ideas give better quantitative results.

An essential feature of Eq. (35) is that it predicts that there is a critical value of concentration at which the entropy of an isotropic distribution of rods becomes zero. Below this concentration each rod is frustrated from choosing its orientation independently of its neighbors and must instead bundle with its neighbors. In the Flory theory which is a hybrid lattice-continuum treatment the frustration occurs at approximately $rV_r = 8$ while other purely lattice treatments give approximately $rV_r = 4$.

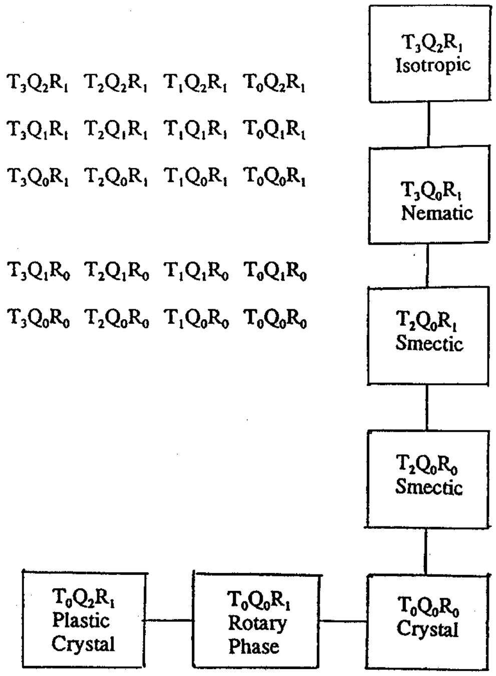
We should explain the heading of this section viz. "liquid crystals/plastic crystals". If we realize that certain degrees of freedom can undergo a phase transition while others do not then we can classify materials according to which degrees of freedom have made a transition [101]. Thus in the isotropic phase the center of mass and the orientation of the rods are liquid-like. A transition to the nematic phase results in restricted orientation but the center of mass still has liquid-like freedom. As we cool further the center of mass losses its freedom and we have a crystal if all three translational degrees of freedom are lost and a smectic A phase if only the translational degree of freedom parallel to the long axis of the rod is lost. A plastic crystal is a material which losses its translational degree(s) of freedom before its orientational degree(s) of freedom. Thus, plastic and liquid crystals form a continuum [102] and a classification on the basis of transitions of "degrees of freedom of molecules" rather than "of molecules" allows us to view the two classes of materials from a unified perspective.

In Fig. 10 we have listed the various kinds of liquid crystals and plastic crystals along with the translational and orientational symmetry. Thus $T_3Q_2R_1$ indicates that the isotropic phase has translational freedom in all three dimensions and complete rotational freedom. $T_0Q_0R_0$ denotes a pure crystal. Usual nomenclature uses O_2 to denote rotation about one angle and O_3 rotation of a rod in 3D space. The rotation (non-rotation) of a rod about its long axis will be denoted by $R_1(R_0)$. A useful feature of a classification is that an empty spot in the classification begs the question as to whether it is necessarily empty or whether the material has not yet been discovered, or whether the classification itself needs modification. This forces one to search in order to answer the question.

Finally we should mention that liquid crystals may be stabilized mainly by favorable energetics of parallel alignment. Steric hindrances need not play the major part. Many thermotropic liquid crystals are of this type as are polymeric liquid crystals formed by placing mesogenic groups in the backbone or as sidegroups of polymer molecules. The Maier–Saupe treatment of liquid crystals did not initially incorporate the Onsager insight but we can do this by proper choice of the self-consistent energy.

The literature on liquid crystals is voluminous. We mention only two recent books by deGennes [103] and Chandrasekar [104].

Liquid crystals have the important feature of combining mobility with structure and allowing transport of chemicals through a structured object.



$T_3Q_2R_1$ $T_2Q_2R_1$ $T_1Q_2R_1$ $T_0Q_2R_1$
$T_3Q_1R_1$ $T_2Q_1R_1$ $T_1Q_1R_1$ $T_0Q_1R_1$
$T_3Q_0R_1$ $T_2Q_0R_1$ $T_1Q_0R_1$ $T_0Q_0R_1$
$T_3Q_1R_0$ $T_2Q_1R_0$ $T_1Q_1R_0$ $T_0Q_1R_0$
$T_3Q_0R_0$ $T_2Q_0R_0$ $T_1Q_0R_0$ $T_0Q_0R_0$
$T_3Q_2R_1$ Isotropic
$T_3Q_0R_1$ Nematic
$T_2Q_0R_1$ Smectic
$T_2Q_0R_0$ Smectic
$T_0Q_2R_1$ Plastic Crystal
$T_0Q_0R_1$ Rotary Phase
$T_0Q_0R_0$ Crystal

Fig. 10. A classification of rigid-rod liquid crystals-plastic crystals according to which degrees of freedom have made a transition. T_j means that the center of mass has translational freedom to move in j dimensions. R_1 means that the rod can rotate about its long axis while R_0 means that it cannot. Q_2 means that the rod has the full two degrees of freedom to point in any direction, Q_1 gives one degree of freedom, while Q_0 means fixed orientation. Thus the isotropic to nematic transition is represented by $T_3Q_2R_1 \rightarrow T_3Q_0R_1$, while isotropic to smectic A is represented by $T_3Q_2R_1 \rightarrow T_2Q_0R_1$. A crystal is represented by $T_0Q_0R_0$. No liquid crystal contains Q_2 and no plastic crystal contains T_3. One row in the figure is left empty because Q_2R_0 is an impossible description. An empty spot in the classification begs the question: has the material not yet been found, or does the classification need modification? We can enlarge the classification by adding I_k to the groups where k enumerates different internal states.

2.2.2. Glass transition/sol–gel transition

The Onsager observation that the formation of the nematic phase in rigid rod systems is entropy driven allows us to develop an important insight into the nature of polymer glasses. The formula $rV_r = 8$ has been used in the previous section by keeping molecular weight r constant and then increasing the volume fraction, V_r, of rigid rods until the product is 8 at which point the random packing gives way to an ordering of the rods. But we could have equally imagined keeping V_r constant and varying r. Now consider with reference to Fig. 11 a model of a semi-flexible polymer which consists of a sequence of rigid rods connected by perfectly flexible joints. At high temperatures the polymer is very flexible which means that the rods are short and the joints many (one less than the number of rods). As we lower the temperature the rods lengthen so that each polymer molecule is represented by fewer connected rigid rods. The number of flexes for a polymer of r monomers is rf where f is the fraction of monomers that are flexed. For an isomeric state model of the polymer with one lower energy well and two higher ones, $f = 2\exp(-\beta\Delta\varepsilon)/(1 + 2\exp(-\beta\Delta\varepsilon))$ and the rod length is $1/f$ which becomes indefinitely large as T decreases. Since in bulk polymers $V_r \approx 1$ as the temperature is lowered we reach the Flory condition $rV_r = 8$ and the articulated rod system then has the same kind of packing difficulties that occur for liquid

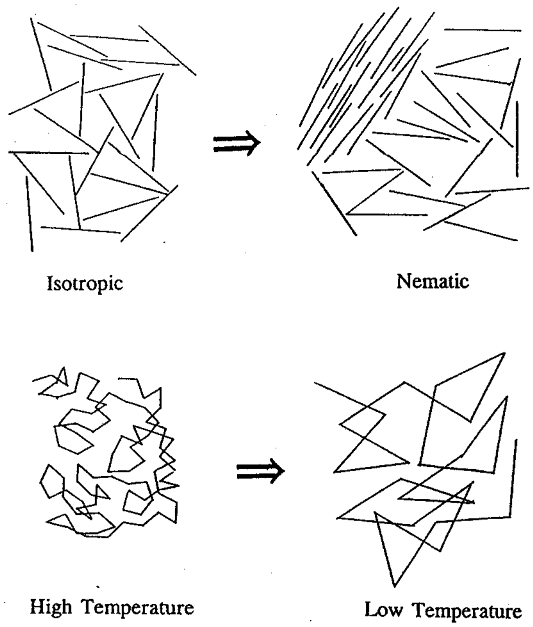


Fig. 11. One can show that the isotropic to nematic liquid crystal (LC) phase transition and polymer glassification occur for the same root cause which is the drastic decrease in configurational entropy. This occurs when we concentrate the rigid rods or cool the semi-flexible bulk polymer. In the first case the rigid rods show frustration beyond a critical concentration which can be avoided by having some of the rods align to form the nematic phase as shown in the upper right hand figure. For glasses we can model the bulk polymer by chains each containing many rigid rod sections. As we cool the bulk polymer from high temperatures the many short rods of each chain become a few long rods of each chain as illustrated and we again reach a concentration where the difficulty in packing the rods causes the polymer molecules to become frustrated from achieving their equilibrium shapes. At this point the rod portions can align to form a LC or a crystal phase, or the chains can become stuck and form the glass phase. The *equilibrium* glass phase results if we substitute for the rigid straight rods rigid but non-straight portions. These non-straight portions cannot pack together to form either LC or crystals (they could only pack parallel by becoming straight, but this would increase their energy for by hypothesis the non-straight portions have the lower energies); they remain stuck and thereby form the glass phase.

crystals. The liquid crystals had three possible alternatives when rV_r exceeded 8. (1) A portion of the material became ordered, i.e. liquid crystalline; (2) if the ordered regions had strong energy preferences there could be an underlying crystal phase which could become the stable phase, and the LC phase would be metastable relative to the crystal phase. This illustrates the important fact that in order to form the LC phase one must not only favor the ordered phase relative to the disordered phase but also the underlying crystal phase must not have energies so strong that they suppress the translational freedom associated with nematic ordering; (3) the final possibility is that the rigid rods get stuck in their randomly ordered phase.

The polymer (articulated rigid rod) system also displays these three options. The rigid rod portions align and form either the liquid crystalline or the crystalline phase; or the rigid rods do not align and they become stuck.

We now argue that the stuck phase is an equilibrium phase, not a metastable phase, and we identify it with the glass phase. To do this we need to distinguish between stiffening and straightening. As we lower the temperature all semi-flexible molecules stiffen. However only certain of the semi-flexible molecule straighten as they stiffen. Polyethylene, for example, is expected to straiten as it stiffens. Its lowest energy state is the perfect zig-zag. However an atactic polystyrene, for example, will have as its lowest energy state one of the large number of random walks possible to it at high temperatures. A bulk system of these molecules when cooled suffers the same reduction in number of configurations as the articulated rod model of a polymer (this statement is a result of actual calculation [12,13]) but there is no ordered phase for it to fall into (The ordered phase requires straight molecules, but they by construction are of high energy.) Such systems form a glass phase of necessity [105].

Thus, the insight that the isotropic to nematic phase transition is entropy driven argues that glass formation in polymers is entropy driven and conversely. The highly successful use of the Onsager insight [83–96] in predicting the properties of liquid crystals argues for the configurational entropy explanation of glass formation and the highly successful configurational entropy explanation of glass formation [12,13,105] argues for the configurational entropy explanation of the isotropic to nematic transition in liquid crystals. It should be noticed that in both liquid crystals and glasses the molecules are frustrated in the same sense as that of Toulise [106]. That is to say, a rigid rod cannot accommodate the energetic preferences of all of its neighbors simultaneously; nor can a stiff (stiff but not straight) polymer.

The above arguments, although they implicate the vanishing of configuration entropy as the explanation of glass formation do not prove that there is an actual transition. For this we must make our best estimate of the functional form of the entropy of a bulk polymer system. When this was done using the Huggins version of the FH lattice model we obtained [12,13] a second-order transition in the Ehrenfest sense. The many comparisons with experiment that were made over the ensuing 40 years were successful. However we must be open to the idea that more accurate statistics would result in a transition that was slightly rounded and that the transition is of third or higher order. This question is still open.

In our original theory of glass formation we postulated that the glass transition occurred when the configurational entropy, S_c, became zero. The theory had S_c, becoming zero at a finite temperature and becoming less than zero at lower temperatures. But if we write this entropy as an integral over a local entropy density s_c,

$$S_c = \int s_c \mathrm{d}x\mathrm{d}y\mathrm{d}z \tag{36}$$

we see that zero entropy implies zero local entropy density everywhere since the entropy density s_c can never be negative. However, the existence of the beta transition below the glass temperature implies that there are pockets of local mobility. Thus, we should view the glass transition as occurring when the packing difficulties experienced locally by the chains first percolates throughout the system [107]. This would occur at temperatures slightly higher than that given by using the condition $S_c = 0$ in the Gibbs–Di Marzio treatment. This idea is developed in analogy to gel formation in polymers. As we continue to introduce cross-links we reach a point (the percolation point [108]) where we have pockets of uncross-linked molecules immersed in a matrix of connected molecules.

Finally we observe that a complete thermodynamic theory of any material requires evaluation of equilibrium properties, kinetic properties, and pattern formation aspects of the kinetics. For glasses the kinetic properties are generally considered to be the most important because the viscosity is always so large near the glass transition, as it must be since the number of allowed configurations is small and flow which is the motion from one allowed configuration to another becomes arrested [12,13,107,109].

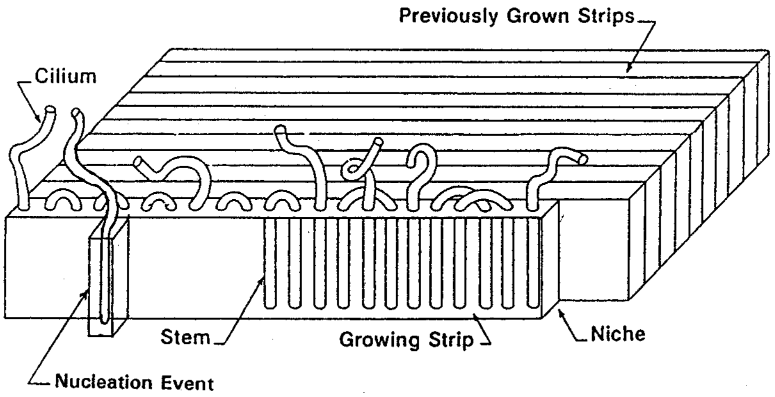


Fig. 12. A polymer lamella formed from low molecular weight polymer in the process of crystallizing from dilute solution. Stems nucleate on the lateral surface with a rate i and then the strip is filled in by lateral growth of rate g. If g is very large the strip is very smooth and the growth rate G perpendicular to the growing face is proportional to i (Regime I growth in which nucleation is the rate determining step). If g is small the surface is corrugated (many strips of few stems each) and the growth rate G is proportional to $(ig)^{1/2}$ (Regime II growth). This figure is meant to illustrate the large number of paths to crystallization that must be considered for a complete theory. What are the proportions of adjacent and next-to-adjacent re-entry? How tight the loops? What fraction of cilia are incorporated into the crystal? Can cilia nucleate adjacent strips? What about the variations in strip thickness? What about variations in stem length? Does the stem lay down as a unit or does it zipper down? A complete theory of polymer crystallization requires that we answer these questions quantitatively and simultaneously.

2.2.3. *Crystallization*

When crystallized from dilute solution polymer crystals grow as thin sheets or lamella with a uniform thickness on the order of 100 Å. The contour length of the polymer is generally much longer than the lamellar thickness so it came as quite a surprise when X-ray data showed that the polymer chains were running perpendicular to the lamellar surfaces and therefore necessarily folding back at the surfaces [110–111]. The straight runs of polymer between the two lamellar surfaces (called stems) are connected by folds at the lamella surfaces. Fig. 12 is illustrative. Polymer crystals formed from the bulk are also lamellar with the stems perpendicular to the lamellar surfaces, but in this case fewer stems fold back into the crystal; some continue into and become part of the amorphous polymer between lamella.

The theory of polymer crystallization was driven by the initially counterintuitive experimental observation of chain folding [110,111]. One would have expected the polymer chains to be completely extended in equilibrium since folds cost energy to create. This suggests that if one could predict growth rate as a function of lamellar thickness it should show a maximum at some finite thickness. This is indeed the case. In 1960, Lauritzen and Hoffman [15] and in 1961, Frank and Tosi [16] developed closely related theories which were able to predict growth rates and lamellar thickness provided that they assumed the lamellar morphology. Since the crystal is a lamella of constant thickness it grows by accreting strips of polymer stems to its perimeter so that the problem is a two dimensional one (one grows both along the strip and outwards). Further it was presumed that the rate determining step was the nucleation step-nucleating an outer strip was a rare event-and once the nucleation event occurred the strip quickly completed its growth. After a relatively long time a new nucleation occurred and the next strip quickly grew; and so on. Thus the problem was reduced to a 1D problem and the flux determined solution which is described in Section 4.1 could be employed. The growth rates α_0 and β_1 of Eq. (41) describe placing the first stem onto the smooth outer strip of the crystal while the α and β describe the stabilization of this stem by chain folding (adding new stems to the side(s) of the initial stem). The nucleation rate, i, is then given by Eq. (47) and the growth rate of the crystal, the rate at which strips are added to the periphery is proportional to i. When the rate constants α, β, α_0 and β_1 are expressed in terms of the bulk and surface free energies of the crystal, then credible predictions of crystal growth are obtained. The cause of the finite lamellar thickness arises from a competition between the placing of the first stem which wants to be short and subsequent strip completion stems which want to be long. For the first stem the lateral surface free energy is positive (unfavorable) and proportional to the stem length; for long stem lengths it overwhelms the negative (favorable) bulk free energy. This is why nucleation events are rare, and they are rarer the longer the stem. The second and subsequent stems that complete the strip have no lateral surface free energy; there is only the favorable bulk free energy and the positive fold energy (end surface free energy). The bulk free energy is proportional to the stem length and therefore favors long stems. Granted the assumption of constant lamella thickness for the growing strip we can then predict growth rate as a function of lamellar thickness, temperature and the energy parameters (bulk energy, lateral surface energy, end surface energy). This growth rate shows a sharp maximum as a function of lamellar thickness and this fact explains lamellar crystallization.

Although successful in predicting growth rates and lamellar thickness as a function of temperature there were several features of the model that needed justification and improvement. The implicit assumption of constant lamellar thickness was addressed and partially justified by the work of Lauritzen and Passaglia [112]. The assumption of tight folds was justified in the work of Di Marzio [69] and of Sanchez and Di Marzio. [17,18]. The assumption of adjacent reentry was partially justified by several arguments [113,114] that developed and expanded an observation of Frank [115]. In order to have non-adjacent reentry one needs to form a loop above the surface of the lamella forming an amorphous phase. If each stem continued into the amorphous melt random walk loops would overfill the space occupied by the amorphous material by a factor of 3 which is impossible [113,114]. This means the amount of adjacent re-entry is of the order of 2/3 or more. The gamblers ruin model [114] of the amorphous–crystalline interface provides valuable insights into its nature. The extreme difficulty of the problem is illustrated in a pair of papers [116,117] which carefully treat short polymers that fold at most once with allowance for adjacent and next to adjacent re-entry and cilia.

Generalizations of the model soon followed. The problems of molecular weight dependence and concentration dependence when crystallizing from dilute solution were examined and partially solved [17,18]. The fractionation that occurred when polymers of different molecular weight were concomitantly crystallized was solved [19].

Applying the work of Hillig [118] on growth of metals to polymers, the formula $G \propto (ig)^{1/2}$ was derived [19]. This is the famous Regime II where both the strip nucleation rate i and the strip fill-in rate g both contribute to the growth rate $G(i, g)$ perpendicular to the strip. In this regime the growth is truly two dimensional. Before the nucleated strip fills-in there is nucleation so that the advancing crystal growth front is highly stepped. In contrast, Regime I nucleation events are so infrequent that strip completion occurs long before the next nucleation event. Finally, we have Regime III where the nucleation rate is so large that the growth rate G is again proportional to i.

The comparison of experiment with theory and the accommodation of one to another has been treated in a series of papers by Hoffman and associates. A recent work by Hoffman and Miller [119] gives the latest developments of what might be called the classical theoretical treatment and contains many references.

The two-volume work of Wunderlich [120], a review by Khoury and Passaglia [121] and a more recent review of Phillips [122] give rich introductions to the complexities of the crystalline morphologies. The fine experimental work emanating from the laboratories of Mandelkern at Florida State, Cheng at Akron and Toda in Japan should also be noted.

2.2.4. Liquid–liquid transitions/polymer blends

Even a cursory review of polymer/solvent and polymer/polymer blends would occupy a full volume, so, we will content ourselves with giving the basic reason behind the phase separation phenomena in these systems and then mention some recent reviews.

Using the lattice model with nearest neighbor energies ε_{ij} the energy ΔE of a blend relative to a reference state of unmixed molecules is for a two-component system

$$\begin{aligned}\Delta E &= (z/2)[2N_1V_2\varepsilon_{12} + N_1V_1\varepsilon_{11} + N_2V_2\varepsilon_{22}] - (z/2)[N_1\varepsilon_{11} + N_2\varepsilon_{22}] \\ &= (z/2)[2N_1V_2\varepsilon_{12} - N_1V_2\varepsilon_{11} - N_2V_1\varepsilon_{22}] = (z/2)N_1V_2(2\varepsilon_{12} - \varepsilon_{11} - \varepsilon_{22}) = N_1V_2\chi kT = N_2V_1\chi kT\end{aligned} \tag{37}$$

where V_j is volume fraction, z is lattice coordination number, N_j is number of monomer units and χ the famous chi-parameter. This formula assumes random mixing and that non-nearest energies are all zero. If we allow non-nearest interaction energies the form of Eq. (37) is unaltered with the εs now being integrals over distance. Now if we imagine the εs to arise from van der Waals potentials we can write $\varepsilon_{ij} = \sigma_1\sigma_2 \int f_{ij}(r)\mathrm{d}r$, with σ_j^2 being Hamaker constants [123–125]. If $f_{ij}(r)$ does not depend on i, j we have

$$\Delta E = (z/2)N_1V_2(\varepsilon_{12} - \varepsilon_{11} - \varepsilon_{22}) = -(z/2)N_1V_2(\sigma_1 - \sigma_2)^2 \int f(r)\mathrm{d}r \tag{38}$$

which shows that as far as the energetics go, like prefers like and only the entropy of mixing favors a mixed system. The entropy of mixing involves three degrees of freedom per center of mass so that it is relatively large, on a per monomer basis, for small polymers but vanishingly small for large molecular weight polymers. Thus the energy contribution to the free energy dominates; for two-component systems of polymers, phase separation is the dominant reality. This is actually observed; most two component polymer systems are phase separated.

Molecularly mixed blends are useful materials and can be achieved in several ways. The first is to use polymers whose energies arise from dipoles, hydrogen bonds, ionic forces-that is energies that are other than van der Waals energies. Another approach is to compatibilize the two polymers by adding diblock copolymers containing the two species one hopes to blend together. This helps to disperse the polymers, sometimes into a molecular mixture, usually into a microphase-separated blend.

The variety of different phase separated modalities has been discussed by Scott and Van Konynenburg [126] for low molecular weight two-component van der Waals fluids. They find nine different regions. Polymers display all the complexities that exist in these blends[2]. We mention a recent review by Han and Akcazu [127] of the important subject of spinodal decomposition in polymer blends.

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[2] And more. because the internal changes can couple in as yet unclassified ways to the transitions arising from those due to mixing.

2.2.5. *Soaps–block copolymers/membranes–micelles–vesicles*

If we attach two incompatible polymers together to form a block copolymer the covalent connection prevents the pieces from traveling too far away from each other and we obtain microphase separation. We then obtain the familiar lamellar, cylindrical and spherical phases which show beautiful regular periodicities on the order of the molecular dimensions. The dimensions tend to vary as the 2/3 power of the molecular weight [128–130]. Thomas and associates have shown that other structures such as gyroids, interpenetrating networks etc. exist as well [37,131–133]. The repeat dimensions of these structures tend to vary as the 2/3 power of the molecular weight. Which structure actually occurs depends on the relative molecular weights of the two blocks, and the system energetics.

Historically, the first amphiphilic materials to be studied were the soaps [33–36]. The structures of soaps parallel those of block copolymers. Thus the neat phase in soaps corresponds to the lamellar phase in polymers; the middle soap phase to the cylindrical polymer phase; the isotropic soap phase to the spherical polymer phase. The more exotic gyroid and interpenetrating phases correspond as well. The difference between block copolymers and soaps is merely a matter of molecular weight.

Free standing membranes, micelles, vesicles and related structures can be thought of as being derived from low molecular weight block copolymers and soaps by adding enough solvent to separate the layers, or cylinders, or spheres from one another. Two options are then possible (1) the structures dissolve in the solvent-uninteresting, (2) the structures separate but retain their integrity-very interesting. They are then called membranes or spherical or cylindrical micelles/vesicles. The route to formation of the above described free-standing structures was described only to emphasize their relation to block copolymers. Usually the route of formation is much different. Membranes can, of course, be formed individually and one of the most biologically significant ways that vesicles and micelles form is through endocytosis [134]. This is explained as follows. In a bilipid membrane, if both sides of the membrane are identical, we expect the membrane to be planar because by symmetry the equilibrium curvature of the bilipid complex equals zero. If the individual halves have a non zero equilibrium curvature the membrane may be close to an instability which could cause buckling. Now, if one side of the membrane is altered by attachment or proximity of other molecules the local equilibrium curvature could become greater/less than zero. This will result in the membrane breaking up and forming spherical vesicles of radii on the order of $1/\rho$. If the principle curvatures are different then cylinder or scrolls [135] are possible. When the other molecules are not spread uniformly but instead are concentrated on a patch of the membrane only this part will bud into vesicles.

The importance of membrane science can be judged by the comment of Nobelist Edeleman [136], who makes the point that surfaces are extremely important in biology, to the effect that in cell processes, surfaces and membranes are all that there is. The sciences of soaps and membranes–micelles/vesicles probably employ more scientists than polymer science and a large amount of their literature is useful to those studying polymers.

Granted the enormous complexity of this subject, it is nonetheless accurate to say that the underlying reason for the existence and complexity of this tenth class of materials resides in the fact that the two incompatible parts of the molecules are trying to phase separate from each other but are prevented from doing so by their connectedness within the molecule. It is this feature that leads to microphase separation and the resultant complexities of soaps, membranes and block copolymers.

2.2.6. *The wetting transition*

In the last five sections we have been concerned only with bulk phases, but since bulk materials have surfaces a complete treatment of these materials must consider surface behavior as well. In a now classic paper on critical point wetting [137] in two-phase fluid mixtures, Cahn has shown that there is a surface phase with its own critical point. This surface phase is not 2D since it has a finite thickness. We must then consider, if even in a rudimentary way, how this transition is evidenced in polymers. It is clear that each of the five bulk phases, singly, or in combinations which are discussed in Section 3, display surface phases that merit study. This is because the Cahn development does not, of logical necessity, require that the phases be liquids. Two applications of these ideas might be:

1. Cheng and colleagues have studied the morphologies of "metastable surface phases" that seem to persist for very long times [138]. Is it possible that these phases are metastable relative to the bulk but stable in the wetting phase?
2. Composto and colleagues have experimentally shown [139,140] a surface enhancement of one of the polymer components in the wetting phase. Can one somehow harvest the enriched wetting phase?

2.2.7. Other transitions

Zwanzig and Lauritzen [141,142] have examined a strictly 2D model of a long molecule that folds back and forth on itself. The molecule consists of straight runs of monomers lying adjacently and connected by tight folds. The transition seems to be second-order.

In the section on liquid crystals we observed that degrees of freedom can have their own transition behavior. Thus the formation of the nematic phase from the isotropic phase can be viewed as a phase transition in the orientation degrees of freedom while the translational degrees of freedom retain their liquid-like character. In plastic crystals the translational degrees of freedom crystallize while the orientational degrees of freedom remain liquid-like. It is suggested that internal degrees of freedom can go through their own transitions while spatial degrees of freedom show no change (there is a science of guage groups that connects the internal modalities to the external ones. There is no reason why these ideas cannot be applied to molecules. See Moriyasu [143], for application to elementary particles and Anderson [144], for a more general treatment in terms of generalized affinities). It is even possible that the momentum degrees of freedom can undergo their own phase transition without a change in the spatial degrees of freedom.

Suppose that we could suddenly change the chemistry. That is to say the A type molecules comprising the material suddenly become B type molecules. Then, obviously thermodynamic transitions can accompany the chemical transformation. The point is that many times we do have a chemical change. An example might be a globular protein that changes from one internal state to another (Section 3.1.1 gives an example of this).

Obviously, we must be open to the possibility that there are more than the ten classes of transitions enumerated above.

3. Coupling of the ten transitions to one another

3.1. Coupling of pairs of transitions

In the matrix of Fig. 13 coupled pairs reside at the intersection of rows and columns. There are (10 ×

Polymer Phase Transitions: Coupled Pairs Reside at the Intersection of Rows and Columns.

	Helix to Random Coil	Polymer Collapse	Polymer-ization	Surface Adsorp-tion	PTM Trans.	Blends	Crystals	Liquid-Crystals, etc.	Glasses/ Gels	Block Co-polymers, Soaps, etc.
Helix to RC	▨									
Polymer Collapse		▨								
Polymer-ization			▨							
Surface Adsorp-tion				▨						
PTM Trans.					▨					
Blends						▨				
Crystals							▨			
Liquid-Crystals								▨		
Glasses/ Gels									▨	
Block Co-polymers, Soaps, etc.										▨

Fig. 13. A matrix with the ten classes of polymer phase transitions listed vertically and horizontally. Each intersection of a row with a column corresponds to a coupling of the two kinds of transitions. There are 45 such (classes of) couplings only a few of which have been studied. Additionally, we have ${}_3C_{10} = 120$ triples of coupled transitions, and so on. Obviously much work is required before polymer phase transitions can be understood in their full generality.

10 − 10)/2 = 45 such pairs. Only a few of them have been investigated. Fewer still have been examined for their relevance to biology or as a technology opportunity. In the following four subsections we shall examine some published examples of coupled pairs of phase transitions.

3.1.1. Sickle cell anemia viewed as a coupling of the polymerization transition and the isotropic to nematic phase transition

Each red blood cell contains millions of haemoglobin molecules at a volume fraction density of about 0.4. In people with the sickle cell trait, under low oxygen pressure, the hemoglobin molecules polymerize to form microtubules which each have the form of a chimney with the bricks of the chimney being globular hemoglobin molecules. From the relation $rV_r = 8$ of Section 2.2.1 we see that when the length/width ratio of the microtubule exceeds 20 the rigid rod microtubules are forced to align forming a nematic phase. Thus, there is a coupling between polymerization and LC formation. These microtubules have a lateral interaction that stabilizes the nematic phase and this, in turn, results in a distortion of the biconcave red blood cell into the sickle shape. In vivo this distortion probably initially occurs when the red cells are making their way through the fine capillaries which distort even healthy cells seeing that their inside diameter is smaller than the cell size. Details of the mathematics can be obtained in the works of Minton [145–149] and of Herzfeld [150].

A similar phenomenon occurs in the formation of phi cell bodies which are associated with cancer of white blood cells. Here certain globular proteins in white blood cells aggregate to form microtubules and the nematic liquid crystalline phase again forms. However in this case the cell wall is weak and the bundle of microtubules punctures the cell wall membrane forming objects which under the microscope look like the greek letter ϕ; hence the name. Descriptions of phi cell bodies are contained in work of Hanker and Giamara [151,152].

3.1.2. The helix to random coil transition near a surface

Some time ago the question was asked of a how the second-order transition of DNA molecules is changed when the DNA is near a surface, and it was concluded that the transition became first-order [153]. However, the treatment was approximate. Quite recently Muthukumar gave an exact treatment of the problem (within the context of path probability methods) of a polypeptide near a surface and showed that even for a single stranded system the transition near the surface can be first-order, even though the polypeptide shows only a diffuse transition away from the surface [154]. A single stranded polypeptide system far from a surface displays a diffuse transition-it occurs over about a ten degree temperature range and has no discontinuities. These results are possibly relevant to the problem of surface induced enzymatic activity or conversely of enzymatic activity that is destroyed by the molecule being near the surface. The point being that the presence of the surface changes the shape of the molecule. Ringsdorf and others [155–157] have shown that enzymatic activity is not always a function of one globular protein. Sometimes a collection of molecules, competing with each other for space, is required.

3.1.3. Two examples from technology; cooling a two-phase glass

First example: Let us cool a two-phase system so that it forms a glass. Then one of the phases can be leached out forming a porous glass, sometimes with very uniform pore sizes. This material is useful, in chromatography for example [158,159].

Second example: Let us cool a bicontinuous two-phase system so that it forms a bicontinuous glass. Then one of the phases can be leached out forming a porous glass. One now heats the glass to collapse the pores. This is the route that is used to make Vicor [160].

3.1.4. The polymer threading a membrane (PTM) transition coupled to the helix–random coil transition

Di Marzio and Ho considered a polypeptide or a DNA molecule threading a membrane [161]. Formally we can solve this problem if in Eq. (1) we replace x_1 and x_2 by $q_1(l_1)$ and $q_2(l_2)$ where the qs are helix–coil partition functions on a per monomer basis. The problem is very difficult when we are dealing with small molecules because the qs are l dependent but in the limit of infinite molecular weight there is a simplification. In this case the major contributions to the partition function are when l_1 and l_2 are both very large. If l_1 and l_2 are very large then the qs are not dependent on l_1, l_2 and the only effect is that in our thermodynamic formulas of Section 2.1.1 we replace the xs by the qs. (A similar treatment holds when the strands adsorb onto the surfaces of the partition separating the two solutions[3]). What we use for q_j depends on our assumptions. We can use the ZUZ model for which we can derive the exact solution even for finite molecular weights or we can use the more realistic treatment of the helix-random coil transition for which we now describe the general character of the transition.

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[3] Actually, all that is required for the polymer to translocate is that the free energy difference per monomer change sign as we lower the temperature. The authors are not aware of any limitation on the number of times this can happen as we cool the system.

Let us model the free energy per monomer unit of the helix to random coil transition by two connected straight line segments of negative slope with the low temperature line being less steep. There is a pair of lines for Region 1 and a pair for Region 2. If these lines are placed together on a free energy versus temperature graph the way they intersect determines the transition behavior. Wherever they cross the ratio of the partition function per molecule goes from 1^+ to 1^- causing a translocation (see Section 3.1). With a little effort we obtain

R1 → H1; R2 → H2
R1 → H2; R2 → H1

R1 → R2 → H1; R1 → R2 → H2; R1 → H1 → H2
R2 → R1 → H2; R2 → R1 → H1; R2 → H2 → H1

R1 → R2 → H1 → H2;   R1 → H1 → R2 → H2;   R2 → R1 → R1 → H2
R2 → R1 → H2 → H1;   R2 → H2 → R1 → H1;   R1 → R2 → H2 → H1

R1 means random coil in Region 1, H2 helix in Region 2, etc. There are 16 different ways for the system to behave as we cool, depending on the choice of the two sets of molecular energy parameters for Regions 1 and 2. Several of them are quite remarkable. R1 → R2 → H1 → H2 means that we start at high temperature with a random coil inside Region 1. On lowering the temperature the polymer translocates to Region 2 as random coil. Then it shuttles back to Region 1 as a helix and finally on lowering the temperature for the third time it goes back into Region 2 as a helix. Obviously there can be much shuttling back and forth across the membrane. In the above it was assumed that the helix is the low temperature form (no inverted transitions) on both sides of the partition.

The translocation transitions are sharp while the transitions on one side of the partition may or may not be sharp depending on the molecular energy parameters.

3.1.5. A comment on the scope of the coupled pair problem

There are three factors which greatly enlarge the scope of the problem beyond what we have already indicated.

First, the kinetics of these coupled systems have been neglected, partially because of the great difficulty associated with solving such systems, but also partially because the format of discussion (our paradigm), i.e. the matrix had to await the discovery of the ten transitions. These kinetics, including pattern formation which can occur at higher growth rates, display richness of structures that have not yet even been classified.

Second, in reality a coupled pair may represent many different transitions. The liquid crystal to crystal transition has (230 space groups) × (1 nematic + 1cholesteric + 7smectic) = 2070 different a priori possible coupled pairs. Many of these can be ruled out as equilibrium states but not as metastable states. They cannot be dismissed without first examining them for their viability.

Third, we should mention that the kinds of molecules that can participate in these transitions is also vast since we can make copolymers and the number of these is exponentially large in n, the degree of polymerization. This combination of many kinds of molecules and many kinds of transitions offers the opportunity for determining and tuning structure via chemical change and conversely.

These observations have importance both in technology and in evolutionary biology.

3.2. The general case displays the vastness of the problem

In Section 3.1 which deals with coupled pairs of transitions we had 10 transitions taken two at a time (${}_2C_{10} = 45$ pairs). For a triplet of transitions we would have ${}_3C_{10} = 120$ triplets of which we have no a priori knowledge and therefore need to be examined. The total number of possible transition systems that need to be examined for viability and possible technology opportunities includes couplings of all orders.

$$ {}_1C_{10} + {}_2C_{10} + {}_3C_{10} + \cdots = (1+1)^{10} - 1 = 1023. \tag{39}$$

When this number is compared to the small number of cases that have actually been studied we see that a vast amount of work remains. The number 1023 is actually a lower bound, as we know from Section 3.1.5, because for example the transition from isotropic to nematic could equally as well been a transition to the cholesteric or any one of the 7 plus smectic phases, or it could have skipped the nematic phase and crystallized into one (at least several) of the 230 crystal space groups.

4. Kinetics and pattern formation enlarge the scope of the problem

Every equilibrium phase that comes to be involves the kinetics of creation of that phase. This fact underlines the importance of kinetic studies. Most kinetic studies lag far behind the equilibrium treatments. This is to be expected since the kinetic problems can be orders of magnitude more difficult, but some progress is being made. Sometimes the equilibrium phase destroys all memory of kinetics but in polymers it is often not the case, as we see below in Section 4.1 where the basic mathematics of one-dimensional crystallization is outlined. Additionally we discuss in Section 4.2, Levinthal's paradox which, if it were not resolvable, would obviate all statistical mechanical treatments of large polymers. Pattern formation is discussed in Section 4.3.

4.1. An example from the list of ten: polymer crystallization

The polymer crystal phase retains memory of its kinetic history in its lamellar thickness (LT) which is frozen in indefinitely if the polymer crystal is formed under conditions of large supercooling. To determine LT we need to kinetic theory of crystallization. As mentioned previously in Section 2. The basics of this is the kinetics [68,69] of 1D crystallization which we now describe.

Fig. 14 describes the model on which we make our calculations. The rate constant for adding a polymer stem to the growing crystal strip of length j is α_j while the rate constant for taking off the jth stem is β_j. From the principle of detailed balance we have

$$\alpha_j/\beta_{j+1} = \exp(-\beta(\mu - \varepsilon_j)) \tag{40}$$

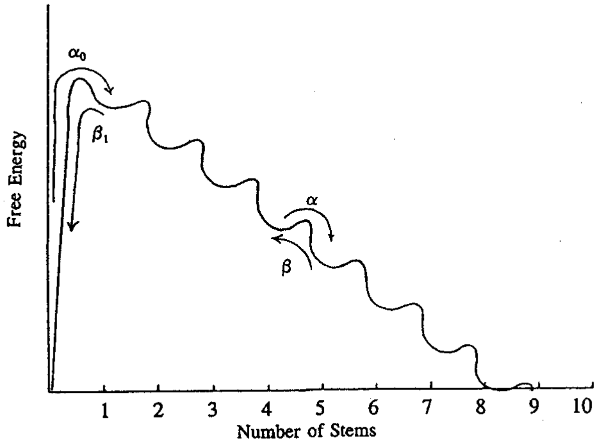

Fig. 14. A free energy diagram for strip growth on the perimeter of a lamella crystal (Regime I). The forward and backward rate constants for the first stem are α_0 and β_1, while the rate constants for all subsequent stems are α and β. The nucleation rate i is compounded from these four rate constants. See text. The strip completion rate g is proportional to $(\alpha - \beta)$.

which relates the rate constants to molecular energetics[4]. If we have N_0 places onto which we can nucleate a polymer (begin to grow a 1D strip of crystal) then the growth equations are

$$dN_0/dt = -(\alpha_0 N_0 - \beta_1 N_1)$$

$$dN_1/dt = (\alpha_0 N_0 - \beta_1 N_1) - (\alpha N_1 - \beta N_2)$$

$$dN_j/dt = (\alpha N_{j-1} - \beta N_j) - (\alpha N_j - \beta N_{j+1}), \qquad j = 2 \text{ to } \infty \tag{41}$$

where we have allowed the rates for nucleation, α_0 and β_1 to differ from the growth rates α and β. There are many approaches to solving these equations for the nucleation and growth of 1D strips of polymer crystals. A method that gives good physical insight is to write down the continuum version of Eq. (41) by expanding $N_j(t) \equiv N(x,t)$ in a Taylor series to obtain

$$\partial N/\partial t = D\partial^2 N/\partial x^2 - v\partial N/\partial x, \qquad D = (\alpha + \beta)(\Delta x)^2/2, \quad v = (\alpha - \beta)\Delta x. \tag{42}$$

The Green's function for this equation

$$N(x,t) = (4\pi Dt)^{-1}\exp(-(x - vt)^2/4Dt) \tag{43}$$

shows that an ensemble of 1D crystals each of length x grows with a mean velocity v while the variance in crystal size grows as $4Dt$.

A particular time independent solution of Eq. (41) called the flux determined solution is of great utility. If $dN_j/dt = 0$, except for N_0 and N_ν we have

$$S_j = (\alpha N_j - \beta N_{j+1}) = S_0, \qquad j = 0 \text{ to } \nu - 1. \tag{44}$$

---

[4] The relevant energies are the bulk free energy, the lateral surface free energy, and the fold-surface free energy.

Multiplying the S_j by $(\beta/\alpha)^j$ and adding together each of the equations we obtain

$$S_0(1-(\beta/\alpha)^\nu)/(1-\beta/\alpha) = \alpha_0 N_0 + (\beta-\beta_1)N_1 - \beta(\beta/\alpha)^{\nu-1}N_\nu \quad (45)$$

while if we add together all equations but the first we have

$$S_0(\beta/\alpha)(1-(\beta/\alpha)^{\nu-1})/(1-\beta/\alpha) = \beta N_1 - \beta(\beta/\alpha)^{\nu-1}N_\nu. \quad (46)$$

Eliminating N_1 from these two equations we obtain for the case where ν is large and N_ν is finite when $\beta/\alpha < 1$ (the growth mode)

$$S_0 = \alpha_0(\alpha-\beta)N_0/(\alpha-\beta+\beta_1) \quad (47)$$

while Eq. (46) itself gives

$$S_0 = N_1(\alpha-\beta) \quad (48)$$

so that from Eq. (44) we obtain

$$N_j = N_{j+1} \quad \text{for } \nu \geq 1. \quad (49)$$

This is the pure-flux-determined-solution (PFDS) and Eq. (47) gives the rate at which nuclei are formed, or equivalently, the rate at which we must augment the nucleation sites to keep N_0 a constant. With both the growth rate $(\alpha-\beta)$ and the nucleation rate S_0 known the problem of 1D crystal growth is solved. The PFDS generalizes the observation of Eq. (4) that the pulse of material drifts or grows with velocity v. These equations have been used to derive formulas for polymer crystal growth [15,16,68,69]. The PFDF displays a first-order transition at the point $\alpha = \beta$ which from Eq. (40) is determined by the chemical potential of the solution and the energy of accretion ε_ν.

The above PFDS exists whenever the system is not clamped at some ν by fixing the value of N_ν. In the general case when we have clamped the system by fixing N_0 and N_ν steady state solutions may not exist and the methods of Lyapunov (Liapunov) need to be employed to determine stability.

Several generalizations of these results should be mentioned. Frank and Tosi [16] give the PFDS for general α_ν, β_ν. Lauritzen et al. [68,69] treat the case where the units being added can be different species. This complicates the problem considerably because the rate constants depend on both what species is being added and to what species we are adding. Also, in the process of unzippering one exposes what was already laid down. N_ν^k which is the number of chains of length ν which have species k at the terminus no longer adequately characterizes the chain. One must express the problem in terms of the variables P_ν^{jk} which is the number of chains of length ν which have species k at the terminus and species j just beneath it at location $\nu - 1$; and so on. By treating polymers in various stages of incorporation into the crystal lamella as being different species one is able to solve the problems of: (1) varying lamellar thicknesses within the same lamella; (2) finite molecular weight [17,18,69]; (3) cocrystallization of polymers of different molecular weights [19]; (4) varying degree of crystallinity [69] and; (5) the amount of adjacent re-entry [69].

4.2. Levinthal's paradox, topological dereliction and metastable states

Levinthal's paradox: Suppose we have a polymer of 100 monomer units and calculate the number of configurations available to it. A reasonable lattice model estimate [162] is 5^{100}. If the monomer units move librate at a rate of 10^{15}/s then it is easy to show that a given configuration chosen at random would be visited about every 10^{43} years. Levinthal's paradox consists in the observation that many globular proteins of this degree of polymerization achieve their globular form in seconds to hours rather than in times greater than the age of the universe [163]. The paradox for globular proteins can be alleviated in several ways. The first way is to recognize that the collapsed phase is not a compact state—it can be a somewhat open structure so that the search for the globular state can take place among the states of the collapsed phase which are orders of magnitude less in number than the number of states constituting the expanded polymer.

The second way is to recognize that states that are of lower energy appear with higher probability because of Boltzmann's law. Let us use a simplified model of the bond energies by assuming that one of the five monomer states has an energy weight of $\exp(-\beta\Delta\varepsilon)$ while the other four have a weight of 1. The fraction of time that the polymer is in the lowest energy state is.

$$f = (\exp(\beta\Delta\varepsilon)/[\exp(\beta\Delta\varepsilon) + 4])^{100} \tag{50}$$

which is to be compared to $5^{-100} \approx 10^{-70}$ were there no energy preferences. For very reasonable values of $\Delta\varepsilon$, $f = 2^{-100} = 10^{-30}$ which is 40 orders of magnitude less. Given this calculation, there is no doubt that globular proteins are among the low energy states.

There is kind of energy funnelling going on as can be seen by reference to Fig. 14 (crystal free energy landscape). The equation that describes the roaming of a phase point in this 1D landscape is the diffusion equation with drift Eq. (42) (chromatography eq). If the wells lay horizontal then the time of escape from a point placed initially in the middle varies as the square of the number of wells but if there is a linear drift in energy levels (a descending stairway) as is shown in Fig. 14 (chromatography eq) then the escape time is proportional to the number of wells. This funneling can also reduce the collapse time by orders of magnitude. A paper by Zwanzig et al. suggested a resolution of the Levinthal paradox along these lines [164].

Another way to avoid the Leventhal paradox is to have a small degree of polymerization (DP) to begin with, since collapse times are exponential in the DP. This suggests that globular proteins are never bigger than they need to be.

Finally, globular proteins can be made by putting together globular protein pieces each of which because of their small DP were produced quickly. Insulin (two pieces) and hemoglobin (four pieces) seem to be examples of this.

Topological dereliction: If we speak in terms of energy or free energy landscapes it is plain that there is much structure to this landscape[5]. The intense study of protein collapse has shown that many times the chain gets hung up or trapped into a state called glassy by some and metastable by others. These are low energy states which can be exited only by climbing energy or entropy barriers. The barriers can be so high that as a practical matter exiting never happens. The process of an isolated polymer becoming trapped in the non-equilibrium regions of its energy landscape is called topological dereliction (TD) by Muthukumar [165]. It is obvious that we can classify proteins into those that suffer TD and those that do not. A rough free energy landscape would favor TD while a smooth free energy landscape favors true minima. TD is also a function of temperature.

Metastable states: Cheng has shown through morphological studies that there are many metastable crystalline morphologies that are quite persistent [138] How they come to be and persist are kinetic questions. One must also ask how they relate to the surface wetting phases that are a necessary adjunct to bulk phases.

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[5] The energy surface is a highly convoluted function of the roughly 10^{23} position coordinates. It consists of many deep wells separated by ridges and peaks. The motion of the phase point on this surface determines the kinetics and metastability.

4.3. Pattern formation

The study of pattern formation is still in its infancy. Spinodal decomposition in two component solutions has been extensively studied [166] but the treatment for a three (and more) component system is extremely difficult. Even more important is the coupling of spinodal decomposition to chemical reactions. The Belosov–Shabotinsky reaction [167] which is a chemical reaction within one phase can be considered to be an example of pattern formation in a one-phase system. In general, chemical reactions can couple to spinodal behavior interestingly [168].

One need not have spinodal decomposition in order to have patterns. Nucleation and growth into a supercooled medium results in snowflakes, for example.

Each of the ten phases and each of the 45 coupled pairs should be examined for pattern formation. Generally one expects pattern formation to occur at the higher growth rates.

It is already useful to have the ten phases plus the 45 coupled pairs as a scheme of classifying a newly observed pattern.

4.4. Added complications arising from the kinetics for coupled pairs of transitions

About the only thing I have discovered here is that there will be many complications. For definiteness let us consider a polymer collapsing near a surface. First, there are initial conditions to worry about. How far is the polymer from the surface and what state of collapse is it in initially? Second, in the absence of external forces the rate of collapse and the rate of approach to the surface are different. Third, in the presence of external forces the rates of collapse and approach are different. Fourth, these complications need to be discussed in the context of spatial as well as temporal variations. It is suggested that the present state of understanding is so weak that computer modeling and experiments are needed to guide whatever theory may be possible. Nevertheless the subject is mentioned here in an attempt to circumscribe the problem of phase transitions in polymers. Sections 2–4 make it quite plain that the scientific community, taken in toto, has been merely strolling around the edge of a field containing a vast number of problems involving polymer phase transitions.

5. Size and shape limitations on the transitions

We must inquire into the limits and controls on the size and the shape of our phases because we will in fact always be dealing with finite systems.

Chemistry is an obvious control. By adjusting chemical potentials the size of the final product as well as the rate of formation can be controlled. Controlling the amount of material available obviously limits phase size as does also material rejected from the growing phase. Time dependent variation of the chemical potentials is an important multi-parameter control variable.

The molecular shape can control the final shape and size of the product [169]. An example is tobaco mosaic virus (TMV). The globular proteins form a tight helix of 17 globular proteins per turn of the helix. The width of the cylindrical TMV is completely determined by the forces and the shape of the one kind of globular protein which comprises the helix, and the length of the cylinder is the same as the length of the RNA threading the core.

A given globular protein has a variety of shapes possible to it. We must be open to the possibility that after a group of proteins assemble to form a structure that there is an annealing of the structure caused by a shuffling of the internal structure of the globular protein comprising the structure. Another method of stabilizing the final structure is by cross-linking or fusing together proteins.

Strain-limited growth also serves to limit the size of crystals. For example, a growing twisted crystal ribbon grows at a finite width and thickness because the strain build-up at the crystal edges arising from the twist raises the strain energy sufficiently high that the free energy difference between crystal and solution changes sign thereby causing the lateral growth to cease.

6. Self-healing systems

A self-healing material is a material with structure such that if its structure is destroyed or damaged it can reconstitute itself by incubation at fixed temperature or by annealing cycles of temperature, pressure, and chemical potentials. Self-healing materials are self-assembling structures whose structures represent stable thermodynamic phases. In equilibrium thermodynamic systems a cycling in time of the intensive variables temperature T, pressure P, and the chemical potentials μ_j can result is healing of materials. A few examples, not restricted to polymers, illustrate the range of possibilities.

6.1. Examples

1. Ice skating rink: After hard use the top layer of ice is melted and then refrozen, thus renewing the surface for the next day's activities. Only temperature cycling is involved.
2. Shape memory alloys: Imagine a bird cage made from a metal shape memory alloy. After an encounter with a prowling cat the cage can be distorted indeed. Not to worry; a temperature cycle will restore the shape of the cage. The bird should be removed first.
3. A covalently cross-linked amorphous polymer above its glass temperature is a rubber and cutting through it with a knife results in permanent injury. But if the cross-links are hydrogen bonds a cut can be erased because the hydrogen bonds can reform. Green slime and silly putty owe their strange properties to renewable cross-links of some kind.
4. The shiny covering on some vinyl floor tiles is a material not far removed from its glass temperature that has both covalent and hydrogen bonding cross-links. Small scratches will partially heal through the reforming of the hydrogen bonds thereby partially renewing the material.
5. The boundary between the notions of self-healing and self-assembly is not distinct. TMV can be disassembled and then reassembled in solution. We call this process self-assembly, but it can be viewed as self healing as well.
6. One can have a self-healing system as well as a self-healing material. An electrolytic capacitor is an example of a self-healing system. After a breakdown due to a surge of high voltage the electrolyte redeposits an oxide coating on the metal electrodes thereby renewing the system.
7. Item 6 uses self-healing materials to renew the system, but a system can be functionally self-healing

and contain no self-healing material. An example is a relay station which when the main relay is damaged automatically throws a new relay in its place.

8. A drag-reducing polymer that is also a living polymer (in dilute solution) is a self-healing system. Under shear and extensive flow conditions the polymer may be degraded but after a quiescent phase it renews itself.

The whole point of this section is that since we have so many thermodynamic phase transitions we should be alert to the possibility of self-healing of these phases as a technology opportunity.

7. Biological self-assembly

7.1. Definitions and examples

Reversible self-assembly: Experimentally one has reversible self-assembly if one can take a structure from a cell or from a part of a living thing and (1) dissolve it in solution so that it loses its structure, (2) reconstitute it, (3) reintroduce it into the cell or living thing and (4) it has recovered its function. We take these four steps to be the test of reversible self-assembly. Some examples of this kind of self-assembled structures are:

1. Tobacco mosaic virus: This is now a textbook example [134,170]. TMV consists of one kind of globular protein wound in a helix about an RNA strand. In a solution of proper pH and ionic strength the one kind of globular protein comprising the helical sheath winds about the central RNA strand. For other ranges of pH and ionic strength the helical sheath can form without the RNA strand.
2. Polymerization of g-actin into the f-actin strands.
3. Hemocyanin: These copper containing molecules which transport oxygen in the blood in some of the snails and stuff do not travel singly but rather they bundle into small crystals of about 120 molecules. They have the shape of short cylinders [171]. Presumably the bundling allows the blood to flow easier.
4. Microtubules: Along with f-actin microtubules provide the scaffolding of cells, maintaining their shape and transporting materials within the cell [134,170]. They are also involved in cell division (mitotic spindle) and the construction of cilia and flagella.
5. Globular proteins [134,170].

Irreversible self-assembly: Globular proteins are of two kinds. (1) Those without chemical cross-links bridging sidegroups. These are the completely reversible globular proteins. (2) Those with chemical cross-links, usually disulfide bonds between cysteine sidegroups, may be irreversible. This introduces the idea that irreversible chemistry can be involved in the process of self-assembly and forces us to expand the notion of self-assembly to include such systems. Examples:

1. Triple-stranded collagen molecules are formed by the assembly of three larger procollagen molecules whose end portions are then cleaved off to form the triple-stranded collagen molecule [134,170]. Another kind of irreversible self-assembly can occur when geometric structures (templates) are involved in the self-assembly process. Examples:
2. Formation of a protein within a ribosome. Here both chemistry and geometry are involved [134,170].
3. Chaperon systems [172]. Here helper molecules are needed in the construction of a structure but are

not part of the final structure. For example, the placing of DNA into the core of a virus usually requires helper molecules.

In the remaining subsections we shall be concerned with mainly reversible self-assembly.

7.2. Classification scheme for a catalogue of self-assembled structures

We list all of the elements that allow us to place the self-assembled item into this or that category of the classification. Classifications are useful for what they contain as well as for what they do not contain. A missing item in the classification suggests a search, either for the item, or for a new classification. The classification categories are (as of this date and subject to improvement)

1. Classification of SA as to which kingdom, phylum, class, order, family, genus or species it exists in.
2. How does SA relate to the genetic code? What are the genes involved in the particular SA process.
3. Self-assembly inside the cell versus SA outside the cell. Examples of SA outside of the cell are sea shells, insect exoskeletons, collagen, silk, hair and horn, haemocyanins.
4. What tissues contain the SA structure?
5. One step SA versus several step SA. A complexity measure of SA might enable us to differentiate between primitive and recent evolutionary successes.
6. The number of different polymer transitions involved in the particular SA process.
7. Reversible versus irreversible SA systems. Covalent chemical reactions induce irreversibility, as do also certain geometrical templates.
8. Does the self-assembly require chaperon molecules?
9. Chemical annealing: after formation a SA structure can become more stabilized by a motion to lower free energy by a kind of shuffling (aging) of its parts.
10. Is the SA structure stable or metastable equilibrium?
11. The relevance of kinetics and/or pattern formation in the particular SA system. The making of a SA structure is like the playing of a symphony. The instruments are the various phase transitions and their expression in time is like the playing of notes. Each SA structure is a musical piece.
12. The relation of SA to hierarchical structures. Rat tail tendon is an example of a 7 level hierarchy.
13. The kinds of molecules involved. Which proteins, RNA, DNA, sugars, other molecules are involved?
14. Classification of SA systems as to function. Regulatory or structural.
15. Classification as to the kind of chemical control. What is controlling the size of the SA structure? The location? The time of expression?
16. Tissue and organ formation as SA.
17. Developmental biology as SA.
18. Other classification distinctions not yet envisaged.

7.3. The catalogue

We list this heading for completeness of our overview. Forming a sensible and complete catalogue will take years. A beginning notion of such a catalogue can be gleened by collecting the examples described in Refs. [134,170,171]. Some of the items in the catalogue will be: (1) the many globular proteins; (2) hair, nails, silk, horn, feathers, seashells; (3) collagen; (4) DNA and RNA; (5) the many viruses; (6) microtubules, cilia and flagella; (7) hemocyanin and; (8) membranes.

7.4. Diseases of self-assembly

Again, we list this heading for completeness of our overview. Forming a sensible and complete catalogue will take years. A listing would help in understanding how control mechanisms work. Perhaps then the disease can be controlled. A list of SA diseases would include sickle-cell anemia, phi cell body cancers, scleroderma, elephant-man disease, other collagen diseases, MS, prion diseases, and others. Viewing a disease as a mistake in the self-assembly process might offer insights into a cure.

8. Self-assembly in technology

We again list this study area for completeness. Just as in the biological case one first needs a basis for classification along the lines of Section 7.2 and one then needs to make a catalogue of actual industrial examples. Because the examples will be catalogued according to the classification there will per force be vacancies (missing entries) in the catalogue which should correspond to technology opportunities. Viewing technology under the paradigm-structure is phase transitions and processing is phase transition kinetics-should provide new insights, especially in polymer technology since there are five additional phase transitions over and above those of other materials and since there is an additional conjugate pair of thermodynamic variables (chain extension and the force on a chain).

8.1. Classification scheme for a catalogue

1. Reversible versus irreversible SA systems. Covalent chemical reactions induce irreversibility.
2. One step SA versus several step SA.
3. The number of different polymer transitions involved in the particular SA process.
4. The relevance of kinetics and/or pattern formation in the particular SA system. The making of a SA structure is like the playing of a symphony. The instruments are the various phase transitions and their expression in time is like the playing of notes. Each SA structure is a musical piece.
5. The relation of SA to hierarchical structures.
6. The kinds of polymer molecules involved.
7. Classification of SA systems as to function.
8. Classification as to the kind of chemical control. What is controlling the size of the SA structure? The location?
9. Chemical annealing: After formation of a SA structure can become more stabilized by a motion to lower free energy by a kind of shuffling (aging) of its parts.
10. The size of the structure(s) nano, micro, macro?
11. Other classification distinctions not yet thought of.

8.2. The catalogue

We list this heading for completeness of our overview. Forming a sensible and complete catalogue will take years. Some of the items in the catalogue will be: (1) microporous glass bands; (2) nanotechnology materials, see below; (3) melt-spun semi-crystalline polymer fibers; (4) flash spinning where the solvent is a volatile vapor; (5) fabrication of thermoplastics; and (6) thin films and membranes.

8.3. Nanotechnology

Self-assembly is one route to nanostructures. Some examples and observations:

1. Block copolymers offer the opportunity of fabricating on a nanoscale spatially regular arrangements of lamella, cylinders or spheres. The scheme is to make the block copolymer and then leach out one of the components, or perhaps decorate one of the components, or perhaps add a solvent which isolates the individual layers, cylinders, or vesicles; etc. Additionally, any of the bicontinuous phases in the classifications of soaps and of polymers mentioned in Section 2.2.5 is a candidate for fabrication into nanostructures.
2. Membranes, either single or in multiple stacks, tubules, which are membranes rolled up into scrolls, and vesicles and micelles are each nanostructures.
3. Microstructures can arise in the formation of crystals or liquid crystals.
4. Polymer blends can display spinodal decomposition on a micro-scale.
5. Each of the five kinds of phase transitions that may occur in the isolated polymer are occurring on a nanoscale since the molecules themselves are nanoscale objects.

These observations suggest that the equilibrium, kinetic and pattern formation aspects of the ten classes of polymer phase transitions and the thousands of possible coupled transitions (see Section 3) may be of some utility to microtechnology and nanotechnology.

9. Implications of our classifications

In viewing polymer science on such a grand and even noble scale as we have done we must be careful not to claim too much. We should not fall into the fallacy of believing what we are doing is the only thing or the most important thing that exists. For this reason it is useful to circumscribe our development by imbedding it in the larger notion of complexity physics. Complexity physics is the science of deriving all the implications of the basic laws of physics. We are thought to be close to deriving the basic laws of physics. However when this happens it will not be the end of science. Complexity physics will never end. The proof of this statement lies in the observation that the number of initial conditions that can be put into the equations of motion are infinite and therefore inexhaustible-the tree of knowledge branches out indefinitely. Indeed complexity physics seems to be entering into a more complex phase-technology is advancing in all directions.

The following abbreviated list of topics in complexity physics circumscribes our work. Cellular automata, symmetry breaking, synergetics, hierarchical structures, emergent reality, pattern formation, non-linear equations (limit cycles, strange attractors, solitons), neural nets, Kaufman nets, localization, deterministic chaos, fractals, autocatalysis, symbiosis, chemotaxis, evolution, nanotechnology. It is clear from this list that phase transitions in polymers is only one aspect of the science of complexity and that self-assembly arising from polymer phase transitions does not exhaust all of self-assembly.

Finally, we would like to suggest that *all evolved life-forms must necessarily be polymeric*. The fact of life on Earth shows the condition is sufficient, but we wish to show it is necessary as well. Although this hypothesis is strongly believed by the author, only a plausibility argument is given.

Let us order all classes of materials by their complexity. Starting from the most complex we first have polymeric organic molecules, then non-polymeric organic molecules, and lastly materials that are non-organic. Life-forms need (1) a certain minimal complexity of form and function, (2) the ability to produce many different kinds of forms often and reproducibly and, (3) an ability to transmit all the information necessary to the forms and functions characterizing the life-form. These three conditions can be achieved only by polymer molecules engaging in the 10 classes of phase transitions described in this work. That is to say, (we presume) the five transitions unique to polymers are necessary. The non-polymer organics do not have this possibility, while the non-organics simply do not have the necessary complexity because non-organic polymers are not nearly as numerous nor are they very stable.

A corollary of the above argument is that mechanisms of evolution cannot be understood without first understanding polymeric self-assembly.

10. Discussion

We have in this paper championed the view that self-assembly in polymer systems is basically nothing more or less than polymer phase transition phenomena. To establish this we first needed to know what phase transitions were available to polymers. We found ten such transitions; five within the isolated polymer molecule and five within collections of molecules. The first five are unique to polymers.

Polymers have a richness of structure that does not exist in any other class of materials because: (1) the number of chemical species in polymers is exponential in the chain length; (2) there are ten classes of phase transitions; and (3) the phase transitions can combine in pairs, triplets etc. to form thousands of (a priori possible) structures.

This extreme richness of possibilities has obstructed our view. Sometimes one does not see the forest for the trees. Instead of being like a bird that always lives in one tree, never straying far from it, we have sought, in intention at least, to soar above the canopy of the forest. This overview allows us to see the interrelations among the transitions and to understand polymer self-assembly as being basically nothing more than polymer phase transition phenomena. We believe that this manuscript contains an overview of the ten polymer transitions and especially of the interrelationships among the transitions that does not exist anywhere else. This statement in no way implies that we are anywhere near solving the many problems of self-assembly. Rather our classification schemes show that many thousands of person-years of work remain. It is just that we now have an overview and even a paradigm on which to base our discussions. The paradigm is that polymer self-assembly is the expression in time and space of combinations of the various polymer phase transitions.

In Section 2 an explanation was given for the occurrence of each of the ten transitions. In Section 2.1.1 we explained why the isolated polymer shows an abundance of phase transitions: essentially, the connectedness of the monomers creates the phase transitions! A significant result is that four of the five isolated molecular transitions can be treated and solved exactly. The treatments, being simple, can be understood by any undergraduate or graduate student who has had a standard statistical mechanics course. The author is aware of no other field that displays so many thermodynamic phase transitions that can be solved exactly.

In Section 2.2.2 it was shown that the isotropic to nematic transition in lyotropic liquid crystals has the same root cause as the glass transition in bulk semi-crystalline polymers. The transition in both cases occurs because of the drastic decrease in configurational entropy. For liquid crystals: the number of ways to arrange rigid rods in space is concentration dependent. As the concentration is raised one reaches a concentration beyond which the rods can no longer pack at random. They are frustrated by their neighbors. Beyond this critical concentration some of the molecules must align. For glasses: as we lower the temperature of a bulk polymer consisting of semi-flexible molecules the molecules stiffen and as a result of the increasing packing difficulties a temperature is reached at which each molecule is frustrated by its neighbors in its attempt to achieve a Boltzmann distribution of shapes. This point of frustration is called the glass temperature. It occurs when the configurational entropy reaches a critically small value (see Fig. 11).

In Section 3 we discussed the possibility of a large number of coupled phase transitions. The number is found to be in the thousands. Very few of them have been investigated in any systematic way. The opportunities for research then are as large as the number of transitions. Examples are given of how coupled pairs of transitions model self assembly in biology and in technology.

Section 4 was to remind us of the importance of kinetics. As one expects, the kinetics are less well developed than the thermodynamics. One dimensional crystallization (polymerization) which forms the mathematical base for polymer crystal growth theory is discussed in some detail. Except for crystallization, kinetic theories lag far behind their equilibrium counterparts for each of the other nine classes of transitions, as do also theories of pattern formation.

The next five sections are bare-bone outlines. They are given for completeness of the structure of the overview, not because they have been built on in any deep or systematic way. Section 5 discussed size and shape limitations on the transitions. The subject is important for biology and nanotechnology where the phases can be quite small. Section 6 discussed self-healing, with examples. Surely there exist many opportunities to invent materials that renew themselves, if as we maintain, self-assembled states are states of stable or metastable equilibrium. Section 7 discussed the important case of biological self-assembly. The need for a catalogue of self-assembled structures is stressed and a classification scheme is suggested. The need for a catalogue of diseases of self-assembly is also noted. Section 8 discussed polymeric self-assembly as a technology opportunity. Finally in Section 9 we discussed the relationship of models of polymer phase transitions to the concepts of complexity physics, and we make two speculative statements; one to the effect that all living beings must necessarily be polymeric, and two that understanding polymer phase transitions is a prerequisite to understanding evolution.

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I wish to thank C.M. Guttman for reading the manuscript. A comprehensive development of the subject of this manuscript requires a book (at a minimum). Such a work would include many references omitted in this paper because of space limitations. I apologize to the researchers, many of them friends, who would be referenced in the larger work.

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